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OM protein - protein search, using sw model

Run on: September 28, 2000, 17:01:17 ; Search time 47.46 Seconds
(without alignments) 220.092 Million cell updates/sec

Title: US-09-142-613-1

Sequence: 1 MAEPROFEFVEMEDHAGODTY.....SPOLATLADVSASLAKOGL 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2295	100.0	W34856	Human tau protein.
2	2262	98.6	R58810	Human tau protein.
3	2223	96.9	W05282	Human tau protein.
4	1983	86.4	W05283	Truncated human tau
5	1719.5	74.9	P91294	Paired helical fil
6	1719.5	74.9	R32708	Human tau-protein.
7	739	32.2	W23331	Neuroblastoma indl
8	733	31.9	W05285	Human tau protein
9	713.5	31.1	W23329	Microtubule-associ
10	593	25.8	R76937	P4F-tau (143-254)
11	563	24.5	R92516	Microtubule-associ
12	551	24.0	W05286	Fragment of microt
13	501	21.8	W05284	Human tau protein
14	364	15.9	R59837	Sequence of human
15	270	11.8	W34876	Human tau protein
16	217	9.5	R98431	Tau40 epitope (res
17	185	8.1	R61330	Peptide phosphoryl
18	185	8.1	W34875	Human tau protein
19	172.5	7.5	R46606	Malerial p15mpj ep
20	172.5	7.5	R46608	Plasmodium falcipa
21	159.5	6.9	R26049	Mef precursor. New
22	157	6.8	R85782	Group B streptococ
23	157	6.8	W40540	Mutant C-beta prot
24	157	6.8	W40538	Mutant C-beta prot
25	157	6.8	W40539	Mutant C-beta prot
26	157	6.8	R85781	Group B streptococ
27	157	6.8	W40537	Group B streptococ
28	157	6.8	W40541	Mutant C-beta prot
29	154	6.7	W43106	C. thermophilum O1
30	153	6.7	W70586	Human SLAP-130. Nu
31	150.5	6.6	W02289	Mouse neuron resti
32	150	6.5	W67883	Human secreted pro
33	150	6.5	R66451	AF-4 protein (enco

34	150	6.5	1210	1	R66450	AF-4 protein (enco
35	148	6.4	818	1	W72035	HSV-2 strain SB5 C
36	148	6.4	1896	1	W72095	HSV-2 strain SB5 C
37	148	6.4	3119	1	W72204	HSV-2 strain SB5 C
38	147.5	6.4	1060	1	Y01540	Trypanosoma cruzi
39	147	6.4	1196	1	R28916	Type III procollag
40	146	6.4	1780	1	W53863	Human gravin polyp
41	145.5	6.3	1313	1	W60213	Spinocerebellar at
42	145	6.3	914	1	W24800	Spinocerebellar at
43	145	6.3	1312	1	W33807	Human ataxin-2. Nu
44	144	6.3	793	1	W73307	Hu60 cell line pro
45	142.5	6.2	452	1	R80041	Human megakaryocyt

ALIGNMENTS

RESULT 1
ID W34856
AC W34856; 27-MAR-1998 (first entry)
DT Human tau protein.
DE Human tau protein.
KW Anticbody; phosphorylated tau protein; paired helical filament;
KW detection; Alzheimer's disease; human.
OS Homo sapiens.
PN MO9734145-A1.
PD 18-SEP-1997.
PE 13-MAR-1997: J00804. — *cyk*
PR 13-MAR-1996: JP-056090.
PA (MITU) MITSUBISHI CHEM CORP.
PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
DR WPI; 97-470978/43.
PT Anticbody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
PS Claim 2, Pages 25-27; 48pp; Japanese.
CC An anticbody, prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
SQ Sequence 441 AA;

Query Match 100.0%; Score 2295; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.3e-152;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAEPROFEFVEMEDHAGODTYGLGDRKQGGTYMHQEDTDAGLKESEPLQPTEDGSEEPG	60
DB	1	MAEPROFEFVEMEDHAGODTYGLGDRKQGGTYMHQEDTDAGLKESEPLQPTEDGSEEPG	60
QY	61	SETSDASTPTAEEDVTAFLVDEGAPKQAAOAPTEIPEGTAEAGIGPTSEDEAAG	120
DB	61	SETSDASTPTAEEDVTAFLVDEGAPKQAAOAPTEIPEGTAEAGIGPTSEDEAAG	120
QY	121	HYTGARVYSKSDGTSGDDKKAKGADGKTKIATPRGAPGQKQANATRIPTAPPAK	180
DB	121	HYTGARVYSKSDGTSGDDKKAKGADGKTKIATPRGAPGQKQANATRIPTAPPAK	180
QY	181	TPPSGGPPKSGDRSGYSSGSPGTPGSRSTPSLPPTPREPKKAVVTPPKSPSSAK	240
DB	181	TPPSGGPPKSGDRSGYSSGSPGTPGSRSTPSLPPTPREPKKAVVTPPKSPSSAK	240
QY	241	SRLOTAPVMPDDKKNVSKTIGSTENLKHOPGGGVQVQIINKLDSNVOSGSGSDNTKKH	300
DB	241	SRLOTAPVMPDDKKNVSKTIGSTENLKHOPGGGVQVQIINKLDSNVOSGSGSDNTKKH	300
QY	301	PGGSGVOIYKPYDLSKYTSKCSLGNIHKKPGGGQYEVASEKLDKRYOSKIGSDNT	360
DB	301	PGGSGVOIYKPYDLSKYTSKCSLGNIHKKPGGGQYEVASEKLDKRYOSKIGSDNT	360
QY	361	THVPDGGNKKIETHTLTFRNNAKAKTDHGAELVYKSPVVGSDTSPRLSNVSGTSGIDMY	420

Db 361 THVGGGKRRKLTFRRENAKAKTDHGAIEYKSPVSGDTSRHLNVSSTGSDMW 420
 |||
 QY 421 DSPOLATLADDEVASASIAKQGL 441
 |||
 Db 421 DSPOLATLADDEVASASIAKQGL 441

RESULT 2
 ID R58810 standard; protein; 441 AA.
 AC R58810;
 DT 27-MAR-1995 (first entry)
 DE Human tau protein.
 KW Tau; cerebrospinal fluid; immunoassay; antibody; detection;
 KM diagnosis; central nervous system; CNS; cytopathies; cytopathy;
 KW Alzheimer's disease.
 OS Homo sapiens.
 PN W09418560-A.
 PD 18-AUG-1994.
 PF 10-FEB-1994; J00196.
 PR 12-FEB-1993; JP-046133.
 PA (TEIJ) TEIJIN LTD
 PI Echui H, Hosoda K, Kobayashi S, Kubota T, Mori H;
 PI Nakamoto T;
 DR WPI; 94-279910/34.
 PT Sandwich immunoassay of tau protein in cerebrospinal fluid - for
 PT diagnosis of Alzheimer's disease and other CNS cytopathies
 PS Claim 1; Page 16-18; 36pp; Japanese.
 CC Detection of the human tau protein (or fragments of it) in samples
 CC of cerebrospinal fluid enables the diagnosis of central nervous
 CC system cytopathies such as Alzheimer's disease. Detection is
 CC performed using labelled antibodies which recognise sites within the
 CC region defined by the amino acid residues 251-441. The antibodies
 CC are preferably polyclonal.
 SO Sequence 441 AA;

Query Match 98.6%; Score 2262; DB 1; Length 441;
 Best Local Similarity 99.1%; Pred. No. 2.7e-150;
 Matches 439; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 MAERROEFWEHEDHAGDGTGLGDRKDGQGYTMH--QEGDIDAGLKESPLQPTEDGSEE 58
 |||
 Db 1 MAERROEFWEHEDHAG--TYGLGDRKDGQGYTMHODQEGDIDAGLKESPLQPTEDGSEE 58
 |||
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPGTTAEAGIGDTPSLEDEA 118
 |||
 Db 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPGTTAEAGIGDTPSLEDEA 118
 |||
 QY 119 AGHTQARMSKSKDGTGSDDKRAKAGDGTATPRGAAPPGQKQANATRIIPAKTPPA 178
 |||
 Db 119 AGHTQARMSKSKDGTGSDDKRAKAGDGTATPRGAAPPGQKQANATRIIPAKTPPA 178
 |||
 QY 179 PKTPSSGEPKSGDRSGTSSPGSGPTGSGSRTPSLPTPTREPKKAAVYRTPEKSSS 238
 |||
 Db 179 PKTPSSGEPKSGDRSGTSSPGSGPTGSGSRTPSLPTPTREPKKAAVYRTPEKSSS 238
 |||
 QY 239 AKSLQIAPVMPDLKNYKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSDNIK 298
 |||
 Db 239 AKSLQIAPVMPDLKNYKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSDNIK 298
 |||
 QY 299 HVPGGGVOIYKRPVDSLKYTSKCGSLGNHKKPGGQVEYKSEKLDKDRVQSKIGSLD 358
 |||
 Db 299 HVPGGGVOIYKRPVDSLKYTSKCGSLGNHKKPGGQVEYKSEKLDKDRVQSKIGSLD 358
 |||
 QY 359 NITHVPGGKNNKIIETHKLTFRRENAKAKTDHGAIEYKSPVSGDTSRHLNVSSTGSD 418
 |||
 Db 359 NITHVPGGKNNKIIETHKLTFRRENAKAKTDHGAIEYKSPVSGDTSRHLNVSSTGSD 418
 |||
 QY 419 MVDSPOLATLADDEVASASIAKQGL 441
 |||
 Db 419 MVDSPOLATLADDEVASASIAKQGL 441

RESULT 3
 ID W05282 standard; Protein; 441 AA.
 AC W05282;
 DT 20-DEC-1996 (first entry)
 DE Human tau protein.
 KW Tau protein; inhibition; modulation; prophylaxis; treatment;
 KW Alzheimer's disease; motor neurone disease; Lewy body disease;
 KW progressive supranuclear palsy; Pick's disease.
 OS Homo sapiens.
 PN W09630766-A1.
 PD 03-OCT-1996.
 PF 25-MAR-1996; E01307.
 PR 27-MAR-1995; GB-006197.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Edwards PC, Harrington CR, Klug A, Roth M, Wilschik CM;
 DR WPI; 96-455570/45.
 DR N-PSDB; T39591.
 PT Assay for inhibitors of tau-tau interaction - used for identifying
 PT cpds., partic. phenothiazine cpds., for treating pathological
 PT tau-tau or neuro:fibrilament aggregation
 PS Example 2; Page 53-54; 97pp; English.
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy.
 SO Sequence 441 AA;

Query Match 96.9%; Score 2223; DB 1; Length 441;
 Best Local Similarity 98.0%; Pred. No. 1.4e-147;
 Matches 434; Conservative 0; Mismatches 5; Indels 4; Gaps 2;

QY 1 MAERROEFWEHEDHAGDGTGLGDRKDGQGYTMH--QEGDIDAGLKESPLQPTEDGSEE 58
 |||
 Db 1 MAERROEFWEHEDHAG--TYGLGDRKDGQGYTMHODQEGDIDAGLKESPLQPTEDGSEE 58
 |||
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPGTTAEAGIGDTPSLEDEA 118
 |||
 Db 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPGTTAEAGIGDTPSLEDEA 118
 |||
 QY 119 AGHTQARMSKSKDGTGSDDKRAKAGDGTATPRGAAPPGQKQANATRIIPAKTPPA 178
 |||
 Db 119 AGHTQARMSKSKDGTGSDDKRAKAGDGTATPRGAAPPGQKQANATRIIPAKTPPA 178
 |||
 QY 179 PKTPSSGEPKSGDRSGTSSPGSGPTGSGSRTPSLPTPTREPKKAAVYRTPEKSSS 238
 |||
 Db 179 PKTPSSGEPKSGDRSGTSSPGSGPTGSGSRTPSLPTPTREPKKAAVYRTPEKSSS 238
 |||
 QY 239 AKSLQIAPVMPDLKNYKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSDNIK 298
 |||
 Db 239 AKSLQIAPVMPDLKNYKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSDNIK 298
 |||
 QY 299 HVPGGGVOIYKRPVDSLKYTSKCGSLGNHKKPGGQVEYKSEKLDKDRVQSKIGSLD 358
 |||
 Db 299 HVPGGGVOIYKRPVDSLKYTSKCGSLGNHKKPGGQVEYKSEKLDKDRVQSKIGSLD 358
 |||
 QY 359 NITHVPGGKNNKIIETHKLTFRRENAKAKTDHGAIEYKSPVSGDTSRHLNVSSTGSD 418
 |||
 Db 359 NITHVPGGKNNKIIETHKLTFRRENAKAKTDHGAIEYKSPVSGDTSRHLNVSSTGSD 418
 |||
 QY 419 MVDSPOLATLADDEVASASIAKQGL 441
 |||
 Db 419 MVDSPOLATLADDEVASASIAKQGL 441

RESULT 4
 W05283 standard; Protein: 390 AA.
 ID W05283;
 AC W05283;
 DE 20-DEC-1996 (first entry)
 DE Truncated human tau protein.
 DE Tau protein; inhibition; modulation; prophylaxis; treatment;
 KM Alzheimer's disease; motor neurone disease; Lewy body disease;
 KM progressive supranuclear palsy; Pick's disease.
 OS Homo sapiens.
 PN W09630766-A1.
 PD 03-OCT-1996.
 PF 25-MAR-1996; E01307.
 PR 27-MAR-1995; GB-006197.
 PR (HOPE) HOFFMANN LA ROCHE & CO AG F.
 PI Edwards PC, Harrington CR, Kling A, Roth M, Wischik CM;
 DR WPI: 96-45557/45.
 PT Assay for inhibitors of tau-tau interaction - used for identifying
 PT cpds., partic. phenothiazine cpds., for treating pathological
 PT tau-tau or neuro-filament aggregation
 PS Claim 11: 97p; English.
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy. This sequence of
 CC the human tau protein is truncated at amino acid residue 390. The
 CC full length protein is given in W05282.
 SQ Sequence 390 AA;

Query Match 86.4%; Score 1983; DB 1; Length 390;
 Best Local Similarity 98.0%; Pred. No. 6.3e-131;
 Matches 384; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

QY 1 MAEPREFEYVMDHAG--TYGLGDRKDDGGYTMH--OEGDTAGLKESPLQPTEDGSEE 58
 DB 1 MAEPREFEYVMDHAG--TYGLGDRKDDGGYTMH--OEGDTAGLKESPLQPTEDGSEE 58
 QY 59 PGESETDAKSTPAEDVTAFLVDEGAPKQAAOPHTETPEGTAEAGIGDTPSLEDDEA 118
 DB 59 PGESETDAKSTPAEDVTAFLVDEGAPKQAAOPHTETPEGTAEAGIGDTPSLEDDEA 118
 QY 119 AGHVTOARWVSKSGDGTSGDDKAKAGADGKTATPRGAAPGQKQANATRIIPAKTPPA 178
 DB 119 AGHVTOARWVSKSGDGTSGDDKAKAGADGKTATPRGAAPGQKQANATRIIPAKTPPA 178
 QY 179 PKTPSSGEPKSGDGRSGYSSPGSPGTSRSTPSLPTPTREPKKAVVATPPKSPSS 238
 DB 179 PKTPSSGEPKSGDGRSGYSSPGSPGTSRSTPSLPTPTREPKKAVVATPPKSPSS 238
 QY 239 AKSRLOTAAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDSNVQSKGSKDNIX 298
 DB 239 AKSRLOTAAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDSNVQSKGSKDNIX 298
 QY 299 HYPGGGSVOIYKPVDSLKVTSKGSLGNIHKKPGGGGVYKSEKLDKDRVQSKIGSLD 358
 DB 299 HYPGGGSVOIYKPVDSLKVTSKGSLGNIHKKPGGGGVYKSEKLDKDRVQSKIGSLD 358
 QY 359 NITHVPGGNNKRIETHTKLTFRENAKAKTDHGA 390
 DB 359 NITHVPGGNNKRIETHTKLTFRENAKAKTDHGA 390

RESULT 5
 P91294 standard; protein: 352 AA.
 ID P91294;
 AC P91294;
 DT 10-MAR-1993 (revised)

DT 18-DEC-1989 (first entry)
 DE Paired helical filament (PHF) core protein.
 KM Paired helical filament (PHF) core protein; Alzheimer's disease;
 KM neurofibrillary tangles.
 OS Homo sapiens.
 PN W08903993-A.
 PD 05-MAY-1989.
 PF 19-OCT-1988; G00867.
 PR 19-OCT-1987; GB-024412.
 PR (MED) Medical Research Council.
 PI Wischik CM, Milstein C, Kling A;
 DR WPI: 89-150854/20.
 PT Paired helical filament core protein - used for providing reagents
 PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
 PT disease.
 PS Disclosure: fig 1; 29p; English.
 CC Paired helical filament core protein was sequenced from DNA obtained
 CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
 CC can be used to make MAb's to the PHF core or nucleotide probes used to
 CC diagnose Alzheimer's disease. The protein sequence QIVYKP (AAs 218-223)
 CC was used to design the probes.
 CC See also N91707.
 SQ Sequence 352 AA;

Query Match 74.9%; Score 1719.5; DB 1; Length 352;
 Best Local Similarity 78.6%; Pred. No. 1.3e-112;
 Matches 348; Conservative 0; Mismatches 2; Indels 93; Gaps 4;

QY 1 MAEPREFEYVMDHAG--TYGLGDRKDDGGYTMH--OEGDTAGLKESPLQPTEDGSEE 58
 DB 1 MAEPREFEYVMDHAG--TYGLGDRKDDGGYTMH--OEGDTAGLKESPLQPTEDGSEE 58
 QY 59 PGESETDAKSTPAEDVTAFLVDEGAPKQAAOPHTETPEGTAEAGIGDTPSLEDDEA 118
 DB 59 PGESETDAKSTPAEDVTAFLVDEGAPKQAAOPHTETPEGTAEAGIGDTPSLEDDEA 118
 QY 119 AGHVTOARWVSKSGDGTSGDDKAKAGADGKTATPRGAAPGQKQANATRIIPAKTPPA 178
 DB 119 AGHVTOARWVSKSGDGTSGDDKAKAGADGKTATPRGAAPGQKQANATRIIPAKTPPA 178
 QY 179 PKTPSSGEPKSGDGRSGYSSPGSPGTSRSTPSLPTPTREPKKAVVATPPKSPSS 238
 DB 179 PKTPSSGEPKSGDGRSGYSSPGSPGTSRSTPSLPTPTREPKKAVVATPPKSPSS 238
 QY 239 AKSRLOTAAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDSNVQSKGSKDNIX 298
 DB 239 AKSRLOTAAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDSNVQSKGSKDNIX 298
 QY 299 HYPGGGSVOIYKPVDSLKVTSKGSLGNIHKKPGGGGVYKSEKLDKDRVQSKIGSLD 358
 DB 299 HYPGGGSVOIYKPVDSLKVTSKGSLGNIHKKPGGGGVYKSEKLDKDRVQSKIGSLD 358
 QY 359 NITHVPGGNNKRIETHTKLTFRENAKAKTDHGAELIYKSPVSGDTPRLSVSTGSLD 418
 DB 359 NITHVPGGNNKRIETHTKLTFRENAKAKTDHGAELIYKSPVSGDTPRLSVSTGSLD 418
 QY 419 MYDSPOLATLADSVASLAKOGL 441
 DB 419 MYDSPOLATLADSVASLAKOGL 441
 QY 441 MYDSPOLATLADSVASLAKOGL 441
 DB 441 MYDSPOLATLADSVASLAKOGL 441

RESULT 6
 R32708 standard; protein: 352 AA.
 ID R32708;
 AC R32708;
 DT 15-JUN-1993 (first entry)
 DE Human tau-protein.
 KM Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
 OS Homo sapiens.
 PN W09303369-A.
 PD 18-FEB-1993.
 PF 03-AUG-1992; U06382.

RESULT 13
 ID W05284 standard; Protein; 95 AA.
 AC W05284;
 DT 20-DEC-1996 (first entry)
 DE Human tau protein core fragment.
 KW tau protein; inhibition; modulation; prophylaxis; treatment;
 KW Alzheimer's disease; motor neurone disease; Lewy body disease;
 KW progressive supranuclear palsy; Pick's disease.
 OS Homo sapiens.
 PN W09630766-A1.
 PD 03-OCT-1996.
 PF 23-MAR-1996; E01307.
 PR 27-MAR-1995; GB-006197.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 DR WPI: 96-455570/45.
 DR N-PSDB: T39592.
 PT Assay for inhibitors of tau-tau interaction - used for identifying
 PT cpds., partic. phenothiazine cpds., for treating pathological
 PT tau-tau or neuro-filament aggregation
 PS Disclosure; Figure 22; 97pp; English.
 CC Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 CC Alzheimer's disease, motor neurone disease, Lewy body disease,
 CC Pick's disease or progressive supranuclear palsy.
 SQ Sequence 95 AA;

Query Match 21.8%; Score 501; DB 1; Length 95;
 Best Local Similarity 100.0%; Pred. No. 1.9e-28;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 297 IKHVPGGGSGVIVKPVDSKVTSCGSLGNIHKKPGGGGVYEVSEKIDFDRVQSKIGS 356
 DB 1 IKHVPGGGSGVIVKPVDSKVTSCGSLGNIHKKPGGGGVYEVSEKIDFDRVQSKIGS 60
 QY 357 LDNITHVPGGNGKKIETHKLTFFRENAKKTGHAE 391
 DB 61 LDNITHVPGGNGKKIETHKLTFFRENAKKTGHAE 95

RESULT 14
 ID R59837 standard; peptide; 67 AA.
 AC R59837;
 DT 04-MAR-1995 (first entry)
 DE Sequence of human microtubule-associated protein tau.
 KW tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
 KW Alzheimer's disease; monoclonal antibody; paired helical filament.
 OS Homo sapiens.
 PN W09413795-A.
 PD 23-JUN-1994.
 PF 10-DEC-1993;
 PR 14-DEC-1992; EP-403403.
 PA (INNO-) INNOGENETICS NV SA.
 PI Mercken M, Van De Voorde A, Vanderveeren M, Vanmechelen E;
 DR WPI: 94-234211/28.
 PT Monoclonal antibody reactive with tau protein - used to develop
 PT prods. for detection of brain diseases involving tau or paired
 PT helical filaments esp. Alzheimer's disease
 PS Claim 6; Page 38; 52pp; English.
 CC Paired helical filament (PHF) tau was partially purified from
 CC postmortem tissue, consisting of grey matter from the frontal
 CC and temporal cortex obd. from Alzheimer patients. The tissue (5-10g)
 CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
 CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at

CC 4 degrees C, the supernatant was adjusted to 1% (w/vol) N-
 CC lauroylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
 CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
 CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
 CC contg. pellet was washed with PBS and resuspended in 1ml of the same
 CC buffer. Hybridomas which produced MAbs reactive with tau protein
 CC were obd. from the spleen cells of Balb/c mice primed s.c. with
 CC partially purified PHF. A MAb which forms an immunological complex
 CC with a human tau protein of sequence in R59837 is secreted by the
 CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
 SQ Sequence 67 AA;

Query Match 15.9%; Score 364; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 4.4e-19;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 RGAAPGQKQANATRPAPKTPPSSGPPKSGRSGXSSPSPCTPGRSRTPS 214
 DB 1 RGAAPGQKQANATRPAPKTPPSSGPPKSGRSGXSSPSPCTPGRSRTPS 60
 QY 215 LPTPTPT 221
 DB 61 LPTPTPT 67

RESULT 15
 ID W34876 standard; peptide; 55 AA.
 AC W34876;
 DT 27-MAR-1998 (first entry)
 DE Human tau protein fragment.
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 OS Homo sapiens.
 PN W09734145-A1.
 PD 18-SEP-1997.
 PF 13-MAR-1997; J00804.
 PR 13-MAR-1996; JP-056090.
 PA (MITU) MITSUBISHI CHEM CORP.
 PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 DR WPI: 97-470978/43.
 PT Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 PS Example; Page 37; 48pp; Japanese.
 CC An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 SQ Sequence 55 AA;

Query Match 11.8%; Score 270; DB 1; Length 55;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 AKTDHGAETIYKPVVSGDTPRHLSNVSTGSDIMWDSFQTLADVEASLAK 438
 DB 1 AKTDHGAETIYKPVVSGDTPRHLSNVSTGSDIMWDSFQTLADVEASLAK 55

Search completed: September 28, 2000, 19:58:13
 Job time: 10616 sec

Fri Sep 29 08:18:19 2000

us-09-142-613-1.rag

Page 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2000, 18:46:58 ; Search time 41.36 Seconds
(without alignments)
163.447 Million cell updates/sec

Title: US-09-142-613-1

Sequence: 1 MAEPROEFVEMEDHAGODTY.....SPQLATLADVSASLANOGL 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 152396 segs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgml_7/prodata/1/1aa/5A_COMB.pep:*
2: /cgml_7/prodata/1/1aa/5B_COMB.pep:*
3: /cgml_7/prodata/1/1aa/6_COMB.pep:*
4: /cgml_7/prodata/1/1aa/PCUS_COMB.pep:*
5: /cgml_7/prodata/1/1aa/Backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1735.5	75.6	352	2	US-08-726-306A-17 Sequence 17, Appl
2	1735.5	75.6	391	2	US-08-726-306A-10 Sequence 10, Appl
3	1735.5	75.6	391	2	US-08-389-011-23 Sequence 23, Appl
4	1735.5	75.6	391	3	US-08-403-917A-23 Sequence 23, Appl
5	1731.5	75.4	351	1	US-08-159-969-2 Sequence 2, Appl
6	593	25.8	112	3	US-08-666-360-1 Sequence 1, Appl
7	416	18.1	160	2	US-08-726-306A-35 Sequence 35, Appl
8	364	15.9	67	2	US-08-389-011-1 Sequence 1, Appl
9	364	15.9	67	3	US-08-403-917A-1 Sequence 1, Appl
10	339	14.8	67	2	US-08-444-951A-1 Sequence 1, Appl
11	188	8.6	40	2	US-08-726-306A-65 Sequence 65, Appl
12	185	8.1	34	2	US-08-602-264A-10 Sequence 10, Appl
13	185	8.1	34	3	US-08-461-018A-10 Sequence 10, Appl
14	174	7.6	33	2	US-08-389-011-2 Sequence 2, Appl
15	174	7.6	33	3	US-08-403-917A-2 Sequence 2, Appl
16	174	7.6	33	2	US-08-444-951A-6 Sequence 6, Appl
17	172.5	7.5	455	4	US-08-726-306A-13 Sequence 13, Appl
18	172.5	7.5	1663	4	US-08-726-306A-13 Sequence 13, Appl
19	165	7.2	33	2	US-08-444-951A-2 Sequence 2, Appl
20	164	7.1	31	2	US-08-444-951A-4 Sequence 4, Appl
21	157	6.8	984	1	US-08-242-932-2 Sequence 2, Appl
22	157	6.8	984	1	US-08-14-481-2 Sequence 2, Appl
23	157	6.8	984	4	US-08-14-481-2 Sequence 2, Appl
24	150	6.5	1187	4	US-08-320-559-28 Sequence 28, Appl
25	150	6.5	1187	3	US-08-545-860D-28 Sequence 28, Appl
26	150	6.5	1187	4	US-08-545-860D-28 Sequence 28, Appl
27	150	6.5	1210	1	US-08-320-559-26 Sequence 26, Appl
28	150	6.5	1210	3	US-08-320-559-26 Sequence 26, Appl

29	150	6.5	1210	4	US-08-726-306A-17	Sequence 26, Appl
30	146	6.4	1780	1	US-08-769-309A-5	Sequence 5, Appl
31	142	6.2	907	3	US-08-783-774-2	Sequence 2, Appl
32	142	6.2	907	4	US-08-783-774-2	Sequence 2, Appl
33	142	6.2	1057	4	US-08-931-820-4	Sequence 4, Appl
34	140.5	6.1	478	3	US-08-155-888-2	Sequence 2, Appl
35	140.5	6.1	1706	2	US-08-459-566-2	Sequence 2, Appl
36	140.5	6.1	1706	2	US-08-399-411-2	Sequence 2, Appl
37	140.5	6.1	1706	3	US-08-516-859A-2	Sequence 2, Appl
38	140	6.1	1057	3	US-08-931-820-1	Sequence 1, Appl
39	139.5	6.1	1442	2	US-08-316-650-12	Sequence 12, Appl
40	139.5	6.1	1442	4	US-08-316-650-12	Sequence 12, Appl
41	139.5	6.1	1588	4	US-08-933-07261-11	Sequence 11, Appl
42	137	6.0	27	2	US-08-244-951A-5	Sequence 5, Appl
43	136.5	5.9	335	2	US-08-405-175A-6	Sequence 6, Appl
44	136.5	5.9	682	1	US-08-642-255-126	Sequence 126, Appl
45	136.5	5.9	682	1	US-08-397-633A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-726-306A-17
Sequence 17, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: Van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henr1
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DINGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-726-306A-17

Query Match 75.6% Score 1735.5; DB 2; Length 352;
Best Local Similarity 79.0%; Pred. No. 1.4e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;


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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-23

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Query Match 75.6%; Score 1735.5; DB 2; Length 391;
Best Local Similarity 79.0%; Pred. No. 1.6e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

QY 1 MAEPROFEVMEHAGDGTGLDRKDGQGYTH--QEGDTDAKLKSPLOTPTEDGSEE 58
DB 40 MAEPROFEVMEHAG--TYGLDRKDGQGYTHQDEGDTDAKLK----- 83
QY 59 PGSETDAKSTPAEDVTAPLVDEGAPGKQAAQPHTEIPEGTTAEAGIGDTPSLEDEA 118
DB 84 -----AEEAGIGDTPSLEDEA 99
QY 119 AGHYTOARMVSKSDGTGSDDKAKAGADGKTATPRGAAPPGQKQGANATRIPAKTPPA 178
DB 100 AGHYTOARMVSKSDGTGSDDKAKAGADGKTATPRGAAPPGQKQGANATRIPAKTPPA 159
QY 179 PKTPSSGEPKSDRSGYSSGSPGTGSGSKRTPSLPTPTPRPKYAVYRTPPKSPSS 238
DB 160 PKTPSSGEPKSDRSGYSSGSPGTGSGSKRTPSLPTPTPRPKYAVYRTPPKSPSS 219
QY 239 AKSLQATAPVMPDLKKNVSKIGSTENLKHOPGGGKVQIINKKLDLSNVQSKGSKDNK 298
DB 220 AKSLQATAPVMPDLKKNVSKIGSTENLKHOPGGGK----- 255
QY 299 HVPGGGVOIYKRPVDSLKYTSKCGSLGNIHKHPGGGOVEYKSEKLDPKRVQSKIGSLD 358
DB 256 -----VOIYKRPVDSLKYTSKCGSLGNIHKHPGGGOVEYKSEKLDPKRVQSKIGSLD 308
QY 359 NITHVPGGKUKKITHHTLPRENAKAKTDHGAELIVYKSPVSGDTSRHLNVSSTGSSID 418
DB 309 NITHVPGGKUKKITHHTLPRENAKAKTDHGAELIVYKSPVSGDTSRHLNVSSTGSSID 368
QY 419 MYDSPQATLADDEVASLAKOGL 441
DB 369 MYDSPQATLADDEVASLAKOGL 391

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RESULT 4
US-08-403-917A-23
Sequence 23, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-23

Query Match 75.6%; Score 1735.5; DB 3; Length 391;
Best Local Similarity 79.0%; Pred. No. 1.6e-123;
Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

QY 1 MAEPROFEVMEHAGDGTGLDRKDGQGYTH--QEGDTDAKLKSPLOTPTEDGSEE 58
DB 40 MAEPROFEVMEHAG--TYGLDRKDGQGYTHQDEGDTDAKLK----- 83
QY 59 PGSETDAKSTPAEDVTAPLVDEGAPGKQAAQPHTEIPEGTTAEAGIGDTPSLEDEA 118
DB 84 -----AEEAGIGDTPSLEDEA 99
QY 119 AGHYTOARMVSKSDGTGSDDKAKAGADGKTATPRGAAPPGQKQGANATRIPAKTPPA 178

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Db 100 AGHTQARWYKSKDGTSGDDKAKAGADGKTKIATPRGAAPPGQKQANATRIIPAKTPPA 159
 QY 179 PKTPSSGGEPPKSGDRSGYSSPGSPGTPGSSRPPLPTPTREPCKVAVVTRPPKSPSS 238
 Db 160 PKTPSSGGEPPKSGDRSGYSSPGSPGTPGSSRPPLPTPTREPCKVAVVTRPPKSPSS 219
 QY 239 AKSLQTAAPVPMPLKKNVSKIGSTENLKHOPGGGVQIINKKLDLSNVQSKGSKDNK 298
 Db 220 AKSLQTAAPVPMPLKKNVSKIGSTENLKHOPGGGVQIINKKLDLSNVQSKGSKDNK 255
 QY 299 HVPGGGVOIYKRPVDSLKVTSCGSLGNHHRPGGGGVYKSEKIDFKDRVQSKIGSID 358
 Db 256 -----VOIYKRPVDSLKVTSCGSLGNHHRPGGGGVYKSEKIDFKDRVQSKIGSID 308
 QY 359 NITHVPGGKNTETKLTFRENAKATDGAELIYKSPVSGDTPRHLSNVSTGSGID 418
 Db 309 NITHVPGGKNTETKLTFRENAKATDGAELIYKSPVSGDTPRHLSNVSTGSGID 368
 QY 419 MVDSPOLATLADDEVASASLAKOG 441
 Db 369 MVDSPOLATLADDEVASASLAKOG 391

RESULT 5
 US-08-159-969-2
 ; Sequence 2, Application US/08159969
 ; Patent No. 5492812
 ; GENERAL INFORMATION:
 ; APPLICANT: Voochels, Paul H.
 ; TITLE OF INVENTION: Diagnostic Method for Alzheimer's
 ; TITLE OF INVENTION: Disease
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/159,969
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/738,778
 ; FILING DATE: 01-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 4697-040
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEFAX: 212 869-8864/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 351 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-159-969-2

Query Match 75.4%; Score 1731.5; DB 1; Length 351;
 Best Local Similarity 79.0%; Pred. No. 2.8e-123;
 Matches 349; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

QY 1 MAERPROFEVMEHDHAGDTGLGDRKDOGDTYMH--QEGDIDAGLKESPLDTPTEDSSE 58

Db 1 MAERPROFEVMEHDHAG--TTGLDRKDOGDTYMHQDEBDTDAGLK----- 44
 QY 59 PGSETSDASTPRAEDVTAPLYDEGAPGQAAOAPTEIPEGTAEAGIGDTPSLDEDA 118
 Db 45 -----AEAGIGDTPSLDEDA 60
 QY 119 AGHTQARWYKSKDGTSGDDKAKAGADGKTKIATPRGAAPPGQKQANATRIIPAKTPPA 178
 Db 61 AGHTQARWYKSKDGTSGDDKAKAGADGKTKIATPRGAAPPGQKQANATRIIPAKTPPA 120
 QY 179 PKTPSSGGEPPKSGDRSGYSSPGSPGTPGSSRPPLPTPTREPCKVAVVTRPPKSPSS 238
 Db 121 PKTPSSGGEPPKSGDRSGYSSPGSPGTPGSSRPPLPTPTREPCKVAVVTRPPKSPSS 180
 QY 239 AKSLQTAAPVPMPLKKNVSKIGSTENLKHOPGGGVQIINKKLDLSNVQSKGSKDNK 298
 Db 181 AKSLQTAAPVPMPLKKNVSKIGSTENLKHOPGGGVQIINKKLDLSNVQSKGSKDNK 216
 QY 299 HVPGGGVOIYKRPVDSLKVTSCGSLGNHHRPGGGGVYKSEKIDFKDRVQSKIGSID 358
 Db 217 -----VOIYKRPVDSLKVTSCGSLGNHHRPGGGGVYKSEKIDFKDRVQSKIGSID 269
 QY 359 NITHVPGGKNTETKLTFRENAKATDGAELIYKSPVSGDTPRHLSNVSTGSGID 418
 Db 270 NITHVPGGKNTETKLTFRENAKATDGAELIYKSPVSGDTPRHLSNVSTGSGID 329
 QY 419 MVDSPOLATLADDEVASASLAKOG 440
 Db 330 MVDSPOLATLADDEVASASLAKOG 351

RESULT 6
 US-08-666-360-1
 ; Sequence 1, Application US/08666360
 ; Patent No. 6008024
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
 ; TITLE OF INVENTION: hydridomas secreting them, antigen recognition of these
 ; TITLE OF INVENTION: antibodies and their applications
 ; NUMBER OF SEQUENCES: 3
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/666,360
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 112 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-666-360-1

Query Match 25.8%; Score 593; DB 3; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.1e-38;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 KGADGKTKIATPRGAAPPGQKQANATRIIPAKTPPRPPSSGGEPPKSGDRSGYSSPGS 202
 Db 1 KGADGKTKIATPRGAAPPGQKQANATRIIPAKTPPRPPSSGGEPPKSGDRSGYSSPGS 60
 QY 203 PGTPGSSRSTPLPTPTREPCKVAVVTRPPKSPSSAKSLQTAAPVPMPLDK 254
 Db 61 PGTPGSSRSTPLPTPTREPCKVAVVTRPPKSPSSAKSLQTAAPVPMPLDK 112

STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-726-306A-65

Query Match 8.6%; Score 198; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 EIVYKSPVSGDTSRHLNYSSTGSDIMVDSPLATLAD 430
DB 1 EIVYKSPVSGDTSRHLNYSSTGSDIMVDSPLATLAD 40

RESULT 12
US-08-602-264A-10
Sequence 10, Application US/08602264A
Patent No. 5837853
GENERAL INFORMATION:
APPLICANT: AKIHIKO TAKASHIMA et al.
TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE
TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-602-264A-10

Query Match 8.1%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 SGRSGYSSPSPGSPETPSRSTPLPPTPREPK 224
DB 1 SGRSGYSSPSPGSPETPSRSTPLPPTPREPK 34

RESULT 13
US-08-461-018A-10
Sequence 10, Application US/08461018A
Patent No. 6071694
GENERAL INFORMATION:
APPLICANT: AKIHIKO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-461-018A-10

Query Match 8.1%; Score 185; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 191 SGRSGTGTGSRSTPSPPTPTREPKVAVRT 224
DB 1 SGRSGTGTGSRSTPSPPTPTREPK 34

RESULT 14
US-08-389-011-2
Sequence 2, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-389-011-2

Query Match 7.6%; Score 174; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 199 SPGSPGTGTGSRSTPSPPTPTREPKVAVRT 231

DB 1 SPGSPGTGTGSRSTPSPPTPTREPKVAVRT 33

RESULT 15
US-08-403-917A-2
Sequence 2, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANNECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-2

Query Match 7.6%; Score 174; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 199 SPGSPGTGTGSRSTPSPPTPTREPKVAVRT 231
DB 1 SPGSPGTGTGSRSTPSPPTPTREPKVAVRT 33

Search completed: September 28, 2000, 19:59:08
Job time: 4330 sec

Fri Sep 29 08:18:20 2000

us-09-142-613-1.rai

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2000, 18:58:10 ; Search time 47.67 Seconds
(without alignments)
572.502 Million cell updates/sec

Title: US-09-142-613-1

Perfect score: 2295
Sequence: 1 MAEPKROEFVEMEDHAGQDTR.....SPQLATLADVSASLAKOGL 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR, 64:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2262	98.6	441	1	ORHUT1 microtubule-associ
2	2011.5	87.6	448	1	ORBOF1 microtubule-associ
3	2003.5	87.3	432	2	JS0306 microtubule-associ
4	1861.5	81.1	686	2	A38235 microtubule-associ
5	1821	79.3	733	2	A45301 microtubule-associ
6	1710.5	74.5	374	2	S46264 microtubule-associ
7	1558.5	67.9	316	1	ORHUT2 microtubule-associ
8	1512	65.9	341	2	B28820 microtubule-associ
9	1508	65.7	364	2	A28820 microtubule-associ
10	1493	65.1	402	1	ORBOF2 microtubule-associ
11	746.5	32.5	472	2	167793 microtubule-associ
12	723	31.5	1830	2	A37981 microtubule-associ
13	719.5	31.4	1828	2	A40115 microtubule-associ
14	717.5	31.3	1825	2	S13507 microtubule-associ
15	713.5	31.1	1824	1	ORHUT microtubule-associ
16	710	30.9	323	2	A55983 microtubule-associ
17	546	23.8	381	2	SS1373 microtubule-associ
18	545	23.7	1152	2	A33183 microtubule-associ
19	523.5	22.8	1125	2	B41206 microtubule-associ
20	481	21.0	125	2	I52650 microtubule-associ
21	475	20.7	1072	2	A37127 microtubule-associ
22	428.5	18.7	982	2	A53253 microtubule-associ
23	403.5	17.6	1224	2	T14007 microtubule-associ
24	278	12.1	242	2	T16349 hypothetical prote
25	193.5	8.4	1560	2	T02885 peroxisome prolif
26	192	8.4	2187	2	T30826 nascent polypeptid
27	184.5	8.0	1211	2	T42230 AF4 protein - mous
28	183.5	8.0	813	2	S70795 vsva protein precu
29	179	7.8	3507	2	T34513 hypothetical prote

30	178	7.8	971	2	T19431 hypothetical prote
31	176	7.7	990	2	I51618 nucleolar phosphop
32	175.5	7.6	704	2	A42680 nucleolus-cytoplas
33	175.5	7.6	858	2	S15762 neurofilament trip
34	175.5	7.6	2441	2	D71623 erythrocyte membra
35	173	7.5	903	2	T19209 probable protein k
36	172.5	7.5	455	2	S31806 emp3 protein pla
37	172	7.5	734	2	B42680 nucleolus-cytoplas
38	172	7.5	744	2	T35192 probable ABC trans
39	171.5	7.5	6642	2	T29018 protein UNC-89 - C
40	169.5	7.4	801	2	T29018 hypothetical prote
41	167.5	7.3	428	2	T24769 hypothetical prote
42	165.5	7.2	839	2	F75518 hypothetical prote
43	165	7.2	1029	2	T30351 mycin-like protein
44	163.5	7.1	825	1	EDBEXD immediate-early pr
45	163.5	7.1	916	2	A27864 neurofilament trip

ALIGNMENTS

RESULT 1
ORHUT1
microtubule-associated protein tau, long splice form - human
N/Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein pa
N/Contains: microtubule-associated protein tau type II; microtubule-associated protei
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1990 #sequence, revision 03-May-1996 #text, change 22-Jun-1999
C/Accession: JS0370; A30217; JN0009; S03796; S26655; S26656; S17302; A43444;
R/Goedert, M.; Spillmann, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A/Title: Multiple isoforms of human microtubule-associated protein tau: sequences and
A/Reference number: JS0370; MID:90380393
A/Accession: JS0370
A/Molecule type: mRNA
A/Residues: 1441 <GOE>
A/Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 7
the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks ins
R/Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A/Title: Cloning and sequencing of the cDNA encoding a core protein of the paired hel
A/Reference number: A30217; MID:88234557
A/Accession: A30217
A/Molecule type: mRNA
A/Residues: 1-44, 103-274, 306-441 <GO2>
A/Accession: A30217
A/Reference number: GB:J03778; MID:9338684; PIDN:AAA0615.1; PID:9338685
A/Cross-references: GB:J03778; MID:9338684; PIDN:AAA0615.1; PID:9338685
R/Lee, G.; Nerve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A/Title: The microtubule binding domain of tau protein.
A/Reference number: JN0009; MID:90180482
A/Accession: JN0009
A/Molecule type: mRNA
A/Residues: 1-44, 103-274, 306-441 <LE>
R/Goedert, M.; Spillmann, M.G.; Potler, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A/Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associ
A/Reference number: S03796; MID:89251564
A/Accession: S03796
A/Molecule type: mRNA
A/Residues: 1-44, 103-441 <GO3>
A/Cross-references: EMBL:X14474; MID:936724; PIDN:CAA32636.1; PID:936725
R/Andreass, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A/Title: Structure and novel exons of the human tau gene.
A/Reference number: S26652; MID:93041757
A/Accession: S26652
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 144-185 <AND>
A/Cross-references: EMBL:X61372; MID:936718; PID:936719
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A/Accession: S26656
A/Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 187-274 <AN2>
 A:Cross-references: EMBL:X61374; NID:G36722; PID:G36723
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
 A:Accession: S26662
 A:Molecule type: DNA
 A:Residues: 371-441 <ANM>
 A:Cross-references: EMBL:X61373
 R:Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
 EMBO J. 10, 2725-2729, 1991
 A:Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's disease
 A:Reference number: S17302; MUID:92007714
 A:Accession: S17302
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 268-274,306-395 <JAK>
 R:Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y.
 J. Biol. Chem. 267, 17047-17054, 1992
 A:Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's disease
 A:Reference number: A43444; MUID:92381012
 A:Accession: A43444
 A:Molecule type: protein
 A:Residues: 2-73,103-130,151-180,191-254,260-269,275-290,299-317,322-340,344-347,354-383
 A:Experimental source: Alzheimer's disease brain
 A:Note: sequence extracted from NCBI backbone (NCBI:P112039)
 C:Comment: This heterogeneous protein, which is found predominantly in cells of the nervous system, is the core protein of the paired helical filament of Alzheimer's disease.
 C:Genetics:
 A:Gene: GDB:MAPT
 A:Cross-references: GDB:119434; OMIM:157140
 A:Map position: 17q21-17q21
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule binding;
 F:1-441/Product: microtubule-associated protein tau, long splice form #status predicted
 F:1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status predicted
 F:1-73,103-441/Product: microtubule-associated protein tau (clone htau37) #status predicted
 F:1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #status predicted
 F:1-44,103-274,306-441/Product: microtubule-associated protein tau, fetal #status predicted
 F:1-44,103-441/Product: microtubule-associated protein tau type II #status predicted <NA
 F:252-282/Domain: MAP2/tau repeat homology <MT1>
 F:283-313/Domain: MAP2/tau repeat homology <MT2>
 F:314-344/Domain: MAP2/tau repeat homology <MT3>
 F:345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 98.6% Score 2262; DB 1; Length 441;
 Best Local Similarity 99.1%; Pred. No. 3.2e-109;
 Matches 439; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 MAEPRQEEVNEEDHAGODTGLGDRKDDGGYTMH--CEGDTDAIGKESPLQTPTEGSGEE 58
 Db 1 MAEPRQEEVNEEDHAG--TYGLGDRKDDGGYTMHODGDDTDAGIKESPLQTPTEGSGEE 58
 QY 59 PGSETSDAKSTFTLADVTAPLVYDEGAPGQAAPHTEIPGTTAEAGIDTDSLEDEA 118
 Db 59 PGSETSDAKSTFTLADVTAPLVYDEGAPGQAAPHTEIPGTTAEAGIDTDSLEDEA 118
 QY 119 AGHTQARMSVSKSDGTGSDKKAKGAGKRTIATPRGAAPGQGNANATRIAPKTPPA 178
 Db 119 AGHTQARMSVSKSDGTGSDKKAKGAGKRTIATPRGAAPGQGNANATRIAPKTPPA 178
 QY 179 PKTPSSGEPKSGDRSGSPGSGRTPTSLTPPTREPRTKVAVVRTPPKSPSS 238
 Db 179 PKTPSSGEPKSGDRSGSPGSGRTPTSLTPPTREPRTKVAVVRTPPKSPSS 238
 QY 239 AKSLQIAPVPMPLKNTKSKTIGSTENKHPGGGKVOIINKKLDLSVQSKGSKDNIX 298
 Db 239 AKSLQIAPVPMPLKNTKSKTIGSTENKHPGGGKVOIINKKLDLSVQSKGSKDNIX 298
 QY 299 HVPGGGSGVQIYKRPVDSLKVTSKGSGIGNHHKPGGGGVEYKSEKLDKDKVQSGIGSLD 358
 Db 299 HVPGGGSGVQIYKRPVDSLKVTSKGSGIGNHHKPGGGGVEYKSEKLDKDKVQSGIGSLD 358

QY 359 NITHVPGGNKKRIETHTKLTRENNAKATDGAETVYKSPVSGDTSRHLNVSSTGSGID 418
 Db 359 NITHVPGGNKKRIETHTLTRENNAKATDGAETVYKSPVSGDTSRHLNVSSTGSGID 418
 QY 419 MVDSPOLATLADSVASLAKOGL 441
 Db 419 MVDSPOLATLADSVASLAKOGL 441

RESULT 2

ORBOT1
 microtubule-associated protein tau, form 1 - bovine
 N:Contains: microtubule-associated protein tau, form 2
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 22-Jun-1999
 C:Accession: A31939; A31914; S04005; A48885; A28173; B33734
 R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
 Mol. Cell. Biol. 9, 1381-1388, 1989
 A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding
 A:Reference number: A31939; MUID:89261765
 A:Accession: A31939
 A:Molecule type: mRNA
 A:Residues: 1-446 <HIM>
 A:Cross-references: GB:M26157; NID:9514913; PIDN:AAA30770.1; PID:9514914
 R:Iqbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
 A:Title: Identification and localization of a tau-peptide to paired helical filaments
 A:Reference number: A33914; MUID:89315854
 A:Accession: A33914
 A:Molecule type: protein
 A:Residues: 28, 'A', '30-38', 'IG', '41', 'AP', '44', 'LK' <IOB>
 A:Experimental source: brain
 A:Note: 40-Piv was also found
 R:Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
 FEBS Lett. 248, 87-91, 1989
 A:Title: Microtubule-associated protein tau. Identification of a novel peptide from b
 A:Reference number: S04005; MUID:89252057
 A:Accession: S04005
 A:Molecule type: protein
 A:Residues: 28, 'A', '30-38', 'IG', '41', 'AP', '44', 'LK' <IO2>
 A:Experimental source: brain
 A:Note: 40-Piv was also found
 R:Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
 J. Biol. Chem. 268, 23512-23518, 1993
 A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are a
 A:Reference number: A48885; MUID:94043150
 A:Accession: A48885
 A:Molecule type: protein
 A:Residues: 'X', '203-208', 'X', '210-211', 'X', '213-216', '238-241', 'X', '243-247', 'X', '404-410', 'X', '4
 A:Experimental source: brain
 A:Note: sequence modified after extraction from NCBI backbone
 R:Alzawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
 J. Biol. Chem. 263, 7703-7707, 1988
 A:Title: Microtubule-binding domain of Tau proteins.
 A:Reference number: A28173; MUID:88227970
 A:Accession: A28173
 A:Molecule type: protein
 A:Residues: 205-218, 'X', '220-223' <A12>
 A:Experimental source: brain
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F:1-44/Product: microtubule-associated protein tau, form 1 #status predicted <BT13>
 F:1-17,193-448/Product: microtubule-associated protein tau, form 2 #status predicted
 F:205-223/Region: microtubule binding #status experimental
 F:229-289/Domain: MAP2/tau repeat homology <MT1>
 F:290-320/Domain: MAP2/tau repeat homology <MT2>
 F:321-351/Domain: MAP2/tau repeat homology <MT3>
 F:352-383/Domain: MAP2/tau repeat homology <MT4>
 F:202,209,242,248,411/Binding site: phosphate (Ser) (covalent) (by proline-directed k
 F:212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status e

Query Match 87.6% Score 2011.5; DB 1; Length 448;

Best Local Similarity 86.7%; Pred. No 2.2e-96;
Matches 399; Conservative 9; Mismatches 21; Indels 31; Gaps 4;

QY 1 MAEPROEFEEVNDHAGODTYGLGDRKDGGYTMH-QEGDITDAGLEKESPLQPTTEDGSEEP 59
Db 1 MAEPRQGEFVNDH-----QGDYTLQDQEGDMDPGKESPLQTPADGSEEP 48
60 GSEFSDAKSTTAEDVTPPLVDEGAPGQAAAQPTPELTPEGTAEAGIGTPTSEEDAA 119
QY 49 GSEFSDAKSTTAEDVTPPLVDEGAPGQAAAQPAETPEGTAAEAGIGTPTSEEDAA 108
Db 120 GHVYQARVYSKNDGTGSDKKKAGADGK--TKATPPGAAPPGGQGANTRIPAKTP 177
QY 109 GHVYQARVYSKNDGTGSDKKKAGADGKPGTKITPPGAAPPGGQGANTRIPAKTP 168
Db 178 APTKPPS-----GEPPKSGDRSGYSSPGSPGTGSRTPSPLETPPTR 221
QY 169 TPKSPATMQVQKPPAPGAKSGESGSGDRSGYSSPGSPGTGSRTPSPLETPPTR 228
QY 222 EPKVAAYVTRTPPKSPSSAKSRQLQTPAPVMPDLKVKYSIGSTENLKHDPGGGKVOILNKK 281
Db 229 EPKVAAYVTRTPPKSPSSAKSRQLQAPGMPDLKVKYSIGSTENLKHDPGGGKVOILNKK 288
QY 282 LDLSNVOSKCGSKNIRKVPGGGSVOIYKRPVDSLKYTKSGSLGNIHKKGGGVVEKS 341
Db 289 LDLSNVOSKCGSKNDIKRHPGGGSVOIYKRPVDSLKYTKSGSLGNIHKKGGGVVEKS 348
QY 342 EKLDPKDVOQKIGSLDITVHPGGGNKKIETHKLTFFENAKAKTDGAETLYKSPVVS 401
Db 349 EKLDPKDVOQKIGSLDITVHPGGGNKKIETHKLTFFENAKAKTDHGAETLYKSPVVS 408
QY 402 DTPPHLSNVSGSIDMVDSPQLATLADDEVASLAKGGL 441
Db 409 DTPPHLSNVSGSIDMVDSPQLATLADDEVASLAKGGL 448

RESULT 3
JS0306 microtubule-associated protein tau - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
R:Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.
A:Title: Developmentally regulated expression of specific tau sequences.
A:Reference number: JS0306; MUID:90180457
A:Accession: JS0306
A:Molecule type: mRNA
A:Residues: 1-432 <KOS>
A>Note: the sequence shown is from adult rat brain
A>Note: The partial sequence from fetal rat brain is lacking residues 266-296; the fetal
R:Kanal, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.;
J. Cell Biol. 109, 1173-1184, 1989
A:Title: Expression of multiple tau isoforms and microtubule bundle formation in fibroblasts
A:Reference number: A33574; MUID:89359509
A:Accession: A33574
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-432 <KAN>
A>Note: A variant lacking residues 63-91 was also found
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F:243-273/Domain: MAP2/tau repeat homology <KTI>
F:274-304/Domain: MAP2/tau repeat homology <KTI>
F:305-335/Domain: MAP2/tau repeat homology <KTI>
F:336-367/Domain: MAP2/tau repeat homology <KTI>
F:262-313/Distal: MAP2/tau repeat homology <KTI>
F:347/Binding site: phosphate (Ser) (covalent) *status predicted

Query Match 87.3%; Score 2003.5; DB 2; Length 432;
Best Local Similarity 88.1%; Pred. No. 5.3e-96;

	Matches	392;	Conservative	15;	Mismatches	21;	Indels	17;	Gaps	3;
OY	1	MAEPROEFEEVMDHAGDQTYGLGDRKDOGCTM--HQEGDIDAGLKESPLDTPTEDGSEE	58							
Dd	1	MAEPRQEDTIEDDAGD-----YTMQDDQGDGDHGLKESPPOPPADDGSEE	47							
OY	59	PGESESDAKSTPTAEDVTAPLVDEGAPGKAQAAPHTEIPFGTAEEAGIGDTPSLEDEA	118							
Dd	48	PGESESDAKSTPTAEDVTAPLVDERAPDKATASHTEIPGTTAAEAGIGDTPNMEQA	107							
OY	177	PAKPTPSSGGPEPKSGDRSGYSPPGSPGCTPGSRSTRPSLPPTPREPKXAVVTRPESP	236							
Dd	168	PSPTKPPSGGPPEPKSGEISGYSPPGSPGCTPGSRSTRPSLPPTPREPKXAVVTRPESP	227							
OY	237	SSAKSLRLOTAVPMPDLKNVSKTGSTENLKHOPGGGVQVLIINKLDSNVOSCGSKDN	296							
Dd	228	SASKSLRLOTAVPMPDLKNVSKTGSTENLKHOPGGGVQVLIINKLDSNVOSCGSKDN	287							
OY	297	IKHYVGGSVQIYVKPYDLSKYTSKCGSLGINHHKPGGGGVYEKSEKLDFDYRKSIKS	356							
Dd	288	IKHPGGSSVQIYVKPYDLSKYTSKCGSLGINHHKPGGGGVYEKSEKLDFDYRKSIKS	347							
OY	357	LDMITHVBGGNKKIETHKLTFRENAKAKTDHGAEIYYKSPVSGDISPRHLSNVSTGS	416							
Dd	348	LDMITHVBGGNKKIETHKLTFRENAKAKTDHGAEIYYKSPVSGDISPRHLSNVSTGS	407							
OY	417	IDMVDSPOLATLADEVSAKOGU 441								
Dd	408	IDMVDSPOLATLADEVSAKOGU 432								
RESULT	4									
A38235		microtubule-associated protein, 110k tau - rat								
C:Species:	Rattus norvegicus (Norway rat)									
C:Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999									
C:Accession:	A38235									
R:Goedert, M.; Spillantini, M.G.; Crowther, R.A.										
A:Title:	Cloning of a big tau microtubule-associated protein characteristic of the pe									
A:Reference number:	A38235; PMID:92179305									
A:Accession:	A38235									
A:Molecule type:	mRNA									
A:Residues:	1-686 <GOE>									
A:Cross-references:	GB:W84156; NID:g207157; PIDN:AAA42204.1; PID:g207158									
A>Note:	Sequence extracted from NCBI backbone (NCBIN:87358, NCBIPI:87359)									
C:Superfamily:	microtubule-associated protein tau; MAP2/tau repeat homology									
C:Keywords:	alternative splicing; microtubule binding; tandem repeat									
F:497-577/Domain:	MAP2/tau repeat homology <MT1>									
F:528-558/Domain:	MAP2/tau repeat homology <MT2>									
F:553-589/Domain:	MAP2/tau repeat homology <MT3>									
F:590-621/Domain:	MAP2/tau repeat homology <MT4>									
Query Match	81.1%; Score 1861.5; DB 2; Length 686;									
Best Local Similarity	55.9%; Pred. No. 1.ee-88;									
Matches 391; Conservative	15; Mismatches 22; Indels 271; Gaps 4;									
OY	1	MAEPROEFEEVMDHAGDQTYGLGDRKDOGCTM--HQEGDIDAGLKESPLDTPTEDGSEE	58							
Dd	1	MAEPRQEDTIEDDAGD-----YTMQDDQGDGDHGLKESPPOPPADDGSEE	47							
OY	59	PGESESDAKSTPTAEDVTAPLVDEGAPGKAQAAPHTEIPFGTAEEAGIGDTPSLEDEA	118							
Dd	48	PGESESDAKSTPTAEDVTAPLVDERAPDKATASHTEIPGTTAAEAGIGDTPNMEQA	107							
OY	177	PAKPTPSSGGPEPKSGDRSGYSPPGSPGCTPGSRSTRPSLPPTPREPKXAVVTRPESP	236							
Dd	168	PSPTKPPSGGPPEPKSGEISGYSPPGSPGCTPGSRSTRPSLPPTPREPKXAVVTRPESP	227							
OY	237	SSAKSLRLOTAVPMPDLKNVSKTGSTENLKHOPGGGVQVLIINKLDSNVOSCGSKDN	296							
Dd	228	SASKSLRLOTAVPMPDLKNVSKTGSTENLKHOPGGGVQVLIINKLDSNVOSCGSKDN	287							
OY	297	IKHYVGGSVQIYVKPYDLSKYTSKCGSLGINHHKPGGGGVYEKSEKLDFDYRKSIKS	356							
Dd	288	IKHPGGSSVQIYVKPYDLSKYTSKCGSLGINHHKPGGGGVYEKSEKLDFDYRKSIKS	347							
OY	357	LDMITHVBGGNKKIETHKLTFRENAKAKTDHGAEIYYKSPVSGDISPRHLSNVSTGS	416							
Dd	348	LDMITHVBGGNKKIETHKLTFRENAKAKTDHGAEIYYKSPVSGDISPRHLSNVSTGS	407							
OY	417	IDMVDSPOLATLADEVSAKOGU 441								
Dd	408	IDMVDSPOLATLADEVSAKOGU 432								

QY 125 ----- 124
 Db 168 QPLGRPEDEVRSHAPASLLWQESPQKAWGKRLGSEEEVDEDITMDESSQESPQAS 227
 QY 125 ----- 124
 Db 228 LAPGATAPQARSVASGVSGETTSIPGFPADGSIPLPADFFSKVSAETQASPPEGTGP 287
 QY 125 ----- 124
 Db 288 SEEGEAPPEFTFHEVEIKASAPKEDLEGATVGAPEAQARQAPSVGKGTKEASLLEPT 347
 QY 125 ----- 162
 Db 348 DKQAPAGLPGRPVSRVQLKARVAGVSKDRGNDENKAKGADGTGAKIAPRGAALPQ 407
 QY 163 KQANATRIIPAKTPPAKTPPSGSGEPKSGDRSGYSFSPGTPGSRSPSLPTPTRE 222
 Db 408 KGTSMNATRIIPAKTPPSGSGEPKSGDRSGYSFSPGTPGSRSPSLPTPTRE 467
 QY 223 PKKVAVTRTPKSPSSAKSRQTAPVPMPLKKNYKSKIGSTENLKHQPGGKQVINKKL 282
 Db 468 PKKVAVTRTPKSPSSAKSRQLQTAPVPMPLKKNYKSKIGSTENLKHQPGGKQVINKKL 527
 QY 283 DLSNVQSKGSKDNKIKHVPGGGSGVQIYKPYDLISKVTSKCSGLNHHKPPGGGVKSE 342
 Db 528 DLSNVQSKGSKDNKIKHVPGGGSGVHYYKPYDLISKVTSKCSGLNHHKPPGGGVKSE 587
 QY 343 KLDFKDVQSKIGSLDNIITHVPGGKNIETHTKLTFRNNAKAKTDHGAELIYKSPVSGD 402
 Db 588 KLDFKDVQSKIGSLDNIITHVPGGKNIETHTKLTFRNNAKAKTDHGAELIYKSPVSGD 647
 QY 403 TSPRHLSNVSTGSDIDMVDSPOLATLADSVASLAKOGL 441
 Db 648 TSPRHLSNVSTGSDIDMVDSPOLATLADSVASLAKOGL 686

RESULT 5

A:Accession: A45301
 Microtubule-associated protein tau - mouse
 N:Alternate names: microtubule binding protein tau
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999
 C:Accession: A45301; S31658
 R:Concise: D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.
 A:Title: Primary structure of high molecular weight tau present in the peripheral neuron
 A:Reference number: A45301; M0ID:92262443
 A:Accession: A45301
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-733 <CON>
 A:Note: This sequence is inconsistent with the nucleotide translation
 A:Note: Sequence extracted from NCBI backbone (NCBI:102045, NCBI:102046)
 R:Kramer, L.; Forstner, M.; Hutter, H.; Hoefler, G.; Kurzbauer, R.; Zatloukal, K.; Kristp
 submitted to the EMBL Data Library, May 1992
 A:Description: First observation of mRNA for a tau-protein from murine liver and kidney
 A:Reference number: S31658
 A:Accession: S31658
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-733 <CON>
 A:Cross-references: EMBL:212133; NID:q54253; PIDN:CA78121.1; PID:q388534
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C:Keyword: microtubule binding; tandem repeat
 F:544-574/Domain: MAP2/tau repeat homology <MT1>
 F:575-605/Domain: MAP2/tau repeat homology <MT2>
 F:606-636/Domain: MAP2/tau repeat homology <MT3>
 F:637-668/Domain: MAP2/tau repeat homology <MT4>

Query Match

79.3%; Score 1821; DB 2; Length 733;

Best Local Similarity 52.4%; Pred. No. 2, 1e-86;
 Matches 391; Conservative 15; Mismatches 22; Indels 318; Gaps 6;

QY 1 MAEROFETMEHAGDITGLDRKDQGYTM-HQEGTDAGLESPLQRTTEGSE 58
 Db 1 MAEROFETMEHAGD-----YTLQDEGDMHGLESPPOPADGAE 47
 QY 59 PGSEISDAKSTPAEDYAPLVDEGAPGQAQAOPHTEIPEGTAEGAGIDGPPSLDEA 118
 Db 48 PGSEISDAKSTPAEDYAPLVDERAPDQAQAOPHTEIPEGTAEGAGIDGPPSLDEA 107
 QY 119 AGHYTQARM----- 127
 Db 108 AGHYTQARM----- 127
 QY 128 ----- 127
 Db 168 SELLRQPGKEGMDRLGSEEEVDEDITVDESSQDSEPPQASLTPGRAPQAGSGVYC 227
 QY 128 ----- 127
 Db 228 GERASVPLTEGVSFLPADFFSKVSAETQASQPEGTPGMEGHEAPETTFHEVEIA 287
 QY 128 ----- 130
 Db 288 STPEKDLLEGATVGVGPEEQAKQTPGSGKGTKEASLQEPKQAPAGLPGRPVSRVP 347
 QY 131 -----SKDGTSDDKA----- 142
 Db 348 QLKARVASKDRGTGNDENKAKTSPSCAKAPSHRPLSPPTLPGSSDPLIKSSPAVSPE 407
 QY 143 -----KGADGKT--KIATPRGAAPQKQANATRIIPAKT 175
 Db 408 PATSPHVSSTPRNSPPTKQMLKGAADGTGAKIATPRGAAPQKQANATRIIPAKT 467
 QY 176 PPAKTPPSGSGEPKSGDRSGYSSPGSPGTSGSRSTPSPPTPREPKVAVTRTPKS 235
 Db 468 TPSPKTPPSGSGEPKSGDRSGYSSPGSPGTSGSRSTPSPPTPREPKVAVTRTPKS 527
 QY 236 PSASAKRLQTAIPPMPLDNVSKISGISTENLKHQPGGKQVINKKLDSNVQSKGSD 295
 Db 528 PSASAKRLQTAIPPMPLDNVSKISGISTENLKHQPGGKQVINKKLDSNVQSKGSD 587
 QY 296 NITHVGGGSGVQIYKPYDLISKVTSKCSGLNHHKPPGGGVKSEKDFDRVQSKIG 355
 Db 588 NITHVGGGSGVQIYKPYDLISKVTSKCSGLNHHKPPGGGVKSEKDFDRVQSKIG 647
 QY 356 SLDNITHVGGGKNIETHTKLTFRNNAKAKTDHGAELIYKSPVSGDTPSRHLSNVSTG 415
 Db 648 SLDNITHVGGGKNIETHTKLTFRNNAKAKTDHGAELIYKSPVSGDTPSRHLSNVSTG 707
 QY 416 SIDMVDSPOLATLADSVASLAKOGL 441
 Db 708 SIDMVDSPOLATLADSVASLAKOGL 733

RESULT 6

A:Accession: S46264
 Microtubule-associated protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999
 C:Accession: S46264
 R:Sadot, E.; Marx, R.; Barg, J.; Behar, L.; Gindburg, I.
 J. Mol. Biol. 241, 325-331, 1994
 A:Title: Complete sequence of 3'-untranslated region of tau from rat central nervous
 A:Reference number: S46264; M0ID:94334997
 A:Accession: S46264
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <SAD>
 A:Cross-references: EMBL:X79321; NID:q517393; PIDN:CAE5889.1; PID:q517394
 C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 F:185-215/Domain: MAP2/tau repeat homology <MT1>

F:216-246/Domain: MAP2/tau repeat homology <MT2>
 F:247-277/Domain: MAP2/tau repeat homology <MT3>
 F:278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 74.5% Score 1710.5; DB 2; Length 374;
 Best Local Similarity 76.9%; Pred. No. 4.6e-81;
 Matches 342; Conservative 14; Mismatches 14; Indels 75; Gaps 4;

QY 1 MAEPROEFVEMDHAGDQDTYGLGDRKDGQGYTM--HQEGTDAGLKESPLQTPREDGSEE 58
 DB 1 MAEPROEFVEMDHAGDQDTYGLGDRKDGQGYTM--HQEGTDAGLKESPLQTPREDGSEE 33
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAPHTPEIGTAAEAGIGDTPSLEDEA 118
 DB 34 -----YTMADQEGDMDHGK----- 33
 QY 119 AGHTQARAVSVSKDGTGSDDKAKGADGKT--KIATPRGAAPGQKQANATRIIPAKTP 176
 DB 50 AGHTQARAVSVSKDGTGSDDKAKGADGKTGAKIATPRGAATPGQKTSNATRIIPAKTT 109
 QY 177 PAPKTPSSGSGPPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPKKAVVATPPKSP 236
 DB 110 PSPKTPSSGSGPPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPKKAVVATPPKSP 169
 QY 237 SSKASRLQTAVPMPDLKAVKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSKDN 296
 DB 170 SSKASRLQTAVPMPDLKAVKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSKDN 229
 QY 297 IKHVPGGGVOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEKIDFDRVQSKIGS 356
 DB 230 IKHVPGGGVOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEKIDFDRVQSKIGS 289
 QY 357 LDNTHVPGGKNKIETHTKLTFRENAKAKTDHGAETIVKSVVSGDTPRHLNVSSTGS 416
 DB 290 LDNTHVPGGKNKIETHTKLTFRENAKAKTDHGAETIVKSVVSGDTPRHLNVSSTGS 349
 QY 417 IDWVDSPOLATLADDEVASLAKQGL 441
 DB 350 IDWVDSPOLATLADDEVASLAKQGL 374

RESULT 7

ORHUT2
 microtubule-associated protein tau, fetal (clone p18) - human

C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997

A:Accession: P00001
 R:Lee, G.; Neyer, R.L.; Kosik, K.S.

A:Title: The microtubule binding domain of tau protein.

A:Reference number: JN0009; MUID:90180482

A:Accession: P00001

A:Molecule type: mRNA

A:Residues: 1-316 <LEE>

A>Note: this sequence differs from a previously reported fetal tau protein sequence only

C:Genetics:

A:Gene: GDB:MAPT; M7B1

A:Cross-references: GDB:119434; OMIM:157140

A:Map position: 17q21-17q22

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule binding;

F:189-219/Domain: MAP2/tau repeat homology <MT1>
 F:189-219/Domain: MAP2/tau repeat homology <MT2>
 F:220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match 67.9% Score 1558.5; DB 1; Length 316;
 Best Local Similarity 90.8%; Pred. No. 2.3e-73;
 Matches 306; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 105 EAGIGDPSLEDEAAGHTQARAVSVSKDGTGSDDKAKGADGKTATPRGAAPGQK 164
 |||

DB 11 EAGIGDPSLEDEAAGHTQARAVSVSKDGTGSDDKAKGADGKTATPRGAAPGQK 70
 QY 165 QANATRIIPAKTPPAPKTPSSGEGPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPK 224
 DB 71 QANATRIIPAKTPPAPKTPSSGEGPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPK 130
 QY 225 KVAAYTRPPKSPSSAKSRLQTAVPMPDLKAVKSKIGSTENLKHQPGGKQVQIINKKLD 284
 DB 131 KVAAYTRPPKSPSSAKSRLQTAVPMPDLKAVKSKIGSTENLKHQPGGK----- 180
 QY 285 SNVQSKGSKDNKIKHVPGGGVOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEK 344
 DB 181 -----VOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEK 219
 QY 345 DFKDRVQSKIGSLDNTHVPGGKNKIETHTKLTFRENAKAKTDHGAETIVKSVVSGDTS 404
 DB 220 DFKDRVQSKIGSLDNTHVPGGKNKIETHTKLTFRENAKAKTDHGAETIVKSVVSGDTS 279
 QY 405 PRHLNVSSTGSDIMVDSPOLATLADDEVASLAKQGL 441
 DB 280 PRHLNVSSTGSDIMVDSPOLATLADDEVASLAKQGL 316

RESULT 8

B28820
 microtubule-associated protein tau type 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

A:Accession: B28820

R:Lee, G.; Cowan, N.; Kirschner, M.

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88095510

A:Accession: B28820

A:Molecule type: mRNA

A:Residues: 1-341 <LEE>

A:Cross-references: GB:M18775; NID:9201114; PID:AAA0165.1; PID:9201115

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>
 F:214-244/Domain: MAP2/tau repeat homology <MT2>
 F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 65.9% Score 1512; DB 2; Length 341;

Best Local Similarity 69.7%; Pred. No. 6e-71;
 Matches 310; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

QY 1 MAEPROEFVEMDHAGDQDTYGLGDRKDGQGYTM--HQEGTDAGLKESPLQTPREDGSEE 58
 DB 1 MAEPROEFVEMDHAGDQDTYGLGDRKDGQGYTM--HQEGTDAGLKESPLQTPREDGSEE 33
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAPHTPEIGTAAEAGIGDTPSLEDEA 118
 DB 34 -----YTMADQEGDMDHGK----- 33
 QY 119 AGHTQARAVSVSKDGTGSDDKAKGADGKT--KIATPRGAAPGQKQANATRIIPAKTP 176
 DB 50 AGHTQARAVSVSKDGTGSDDKAKGADGKTGAKIATPRGAAPGQKTSNATRIIPAKTT 107
 QY 177 PAPKTPSSGSGPPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPKKAVVATPPKSP 236
 DB 108 PSPKTPSSGSGPPKSGDRSGYSSPGSPGTGSRSTPSPPTPREPKKAVVATPPKSP 167
 QY 237 SSKASRLQTAVPMPDLKAVKSKIGSTENLKHQPGGKQVQIINKKLDLSNVQSKGSKDN 296
 DB 168 SSKASRLQTAVPMPDLKAVKSKIGSTENLKHQPGGK----- 205
 QY 297 IKHVPGGGVOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEKIDFDRVQSKIGS 356
 DB 206 -----VOIYKPVLSKVTSGSLGNHHKPGGGQVEVSEKIDFDRVQSKIGS 256
 QY 357 LDNTHVPGGKNKIETHTKLTFRENAKAKTDHGAETIVKSVVSGDTPRHLNVSSTGS 416

Db 257 LDNITHVPGGNNKKTETHTLTFRENAKAKTDHGAELIVKSPVSGDTSRHLNNVSGTGS 316
 QY 417 IDWVDSPOLATLADSVASLAKOG 441
 Db 317 IDWVDSPOLATLADSVASLAKOG 341

RESULT 9

A28820

microtubule-associated protein tau type 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: A28820

R:Lee, G.; Cowan, N.; Kirschner, M.

Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88099510

A:Accession: A28820

A:Residues: 1-364 <LEP>

A:Cross-references: GB:M18776; NID:g201116; PID:AAA0166.1; PID:g201117

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match

Best Local Similarity 65.7%; Score 1508; DB 2; Length 364;

Matches 309; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

QY 1 MAEPPOEFVVDHGGQOTYGLGDRKDDGGYTM--HOGGDTAGIKESPLQTPEDSGSE 58
 Db 1 MADPPOEFVVDHGGQOTYGLGDRKDDGGYTM--HOGGDTAGIKESPLQTPEDSGSE 33
 QY 59 PGSETSDAKSTPTAEVTAFLVDEGAPGQAAPHTPEGTAEAGIGDTPSELEDA 118
 Db 34 -----AEEAGIGDTPSELEDA 49
 QY 119 AGHTVQAMVSKSKDGTGSDKKAGADGKT--KATPPGAAPPOGQGANTRIPAKTP 176
 Db 50 AGHTVQAMVSKSKDGTGSDKKAGADGKT--KATPPGAAPPOGQGANTRIPAKTP 107
 QY 177 PAPKTPSSGEPKSGDSSGYSPPGSPGSRSPSPPTREPKVAVYRTPPKSP 236
 Db 108 PSPKTPSSGEPKSGDSSGYSPPGSPGSRSPSPPTREPKVAVYRTPPKSP 167
 QY 237 SSASRLQTAAPVPMEDLNKVNKSKIGSTENLKHQPGGKVOIINKKLDLSNVOSKGSKN 296
 Db 168 SAKSRLOTAAPVPMEDLNKVNKSKIGSTENLKHQPGGKVOIINKKLDLSNVOSKGSKN 205
 QY 267 IKHVPGGGVOIVKPVLDLKYTSKCGSLGNHHRPGGGQVEVSEKLDKDRVOSKIGS 356
 Db 206 -----VOIVKPVLDLKYTSKCGSLGNHHRPGGGQVEVSEKLDKDRVOSKIGS 256
 QY 357 LDNITHVPGGNNKKTETHTLTFRENAKAKTDHGAELIVKSPVSGDTSRHLNNVSGTGS 416
 Db 257 LDNITHVPGGNNKKTETHTLTFRENAKAKTDHGAELIVKSPVSGDTSRHLNNVSGTGS 316
 QY 417 IDWVDSPOLATLADSVASLAKOG 440
 Db 317 IDWVDSPOLATLADSVASLAKOG 340

RESULT 10

QRBOT2

microtubule-associated protein tau, form 3 - bovine

N:Contains: microtubule-associated protein tau, form 4; microtubule-associated protein t

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996

C:Accession: B31939; A48885; A28173

R:Himler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
 Mol. Cell. Biol. 9, 1381-1388, 1989
 A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind
 A:Reference number: A31939; MUID:89261765

A:Accession: B31939

A:Molecule type: mRNA

A:Residues: 1-402 <HIM>

A:Cross-references: GB:M26157; GB:M26158

R:Paudel, H.K.; Lew, J.; Ali, Z.; Mang, J.H.

J. Biol. Chem. 268, 23512-23518, 1993

A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are e

A:Reference number: A48885; MUID:94043150

A:Accession: A48885

A:Molecule type: Protein

A:Residues: 'X',157-162,'X',164-165,'X',167-170;192-195,'X',197-201,'X',358-364,'X',3

A:Experimental source: brain

A>Note: sequence modified after extraction from NCBI backbone

R:Alzawa, H.; Kawasaki, H.; Murofushi, R.; Kotani, S.; Suzuki, K.; Sakai, H.

J. Biol. Chem. 263, 7703-7707, 1988

A:Title: Microtubule-binding domain of Tau proteins.

A:Reference number: A28173; MUID:88227970

A:Accession: A28173

A:Molecule type: protein

A:Residues: 159-172,'X',174-177 <AI2>

A:Experimental source: brain

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat

F:1-234,297-402/Product: microtubule-associated protein tau, form 3 #status predicted <RT4>

F:101-402/Product: microtubule-associated protein tau, form 5 #status predicted <RT4>

F:159-177/Region: microtubule binding #status experimental

F:213-243/Domain: MAP2/tau repeat homology <MT1>

F:244-274/Domain: MAP2/tau repeat homology <MT2>

F:275-305/Domain: MAP2/tau repeat homology <MT3>

F:306-337/Domain: MAP2/tau repeat homology <MT4>

F:166,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directed k

F:166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status f

Query Match

Best Local Similarity 65.1%; Score 1493; DB 1; Length 402;

Matches 303; Conservative 14; Mismatches 29; Indels 34; Gaps 6;

QY 64 SDAKSTPTAEVTAFLVDEGAPGQAAPHTPEGTAEAGIGDTPSELEDAAGHTV 123
 Db 55 SPKPTPGSSD---PLKTPSSP-----ANCPESSSSPK-----HVS 87
 QY 124 QARVSKSKDGTGSDDKKAGADGK--TKATPPGAAPPOGQGANTRIPAKTPAKT 181
 Db 88 S---VTPTRTGNSGAKEMKVGADGKPGTKATTPRGAAPPOGQGANTRIPAKTPAKT 144
 QY 182 PPSSGEPKSGDRSGYSSPGSPGSRSPSPPTREPKVAVYRTPPSPSSAKS 211
 Db 145 SP--GESGKSGDRSGYSSPGSPGSRSPSPPTREPKVAVYRTPPSPSSAKS 202
 QY 242 RLQTAAPVPMPLKVNKSKIGSTENLKHQPGGKVOIINKKLDLSNVOSKGSNDIKHYV 301
 Db 203 RLQTAAPVPMPLKVNKSKIGSTENLKHQPGGKVOIINKKLDLSNVOSKGSNDIKHYV 262
 QY 302 GGGSVQIVYKPVLDLKYTSKCGSLGNHHRPGGGQVEVSEKLDKDRVOSKIGSLDNIT 361
 Db 263 GGGSVQIVYKPVLDLKYTSKCGSLGNHHRPGGGQVEVSEKLDKDRVOSKIGSLDNIT 322
 QY 362 HVPGGGNNKKTETHTLTFRENAKAKTDHGAELIVKSPVSGDTSRHLNNVSGTGSIDWYD 421
 Db 323 HVPGGGNNKKTETHTLTFRENAKAKTDHGAELIVKSPVSGDTSRHLNNVSGTGSIDWYD 382
 QY 422 SPOLATLADSVASLAKOG 441
 Db 383 SPOLATLADSVASLAKOG 402

RESULT 11

167793
microtubule-associated protein 2, splice form MAP-2c - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Dec-1998
C:Accession: 167793
R:Albaladejo, J.S.; Kalcheva, N.; Shafit-Zagardo, B.
Gene 136, 377-378, 1993
A:Title: Characterization of the transcripts encoding two isoforms of human microtubule
A:Accession: 167793
A:Reference number: 153653; MUID:94124038
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-472 <ALB>
A:Cross-references: GB:LI2563; NID:g348216; PID:g348217
C:Genetics:
A:Gene: GDB:MAP2; MAP2A; MAP2B; MAP2C
A:Cross-references: GDB:118836; OMTM:157130
A:Map position: 2q34-q34
A:Introns: 151/3
C:Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
E:314-344/Domain: MAP2/tau repeat homology <MT1>
E:376-407/Domain: MAP2/tau repeat homology <MT3>


```

Db 1707 -----VTSKCGSLKNIRHPPGGGVYKLEESYKLDKEKAQAKV 1743
QY 335 GSLDNITHVPGGKNIETHKLTFRNNAKAKTIDGAEIYKSPVSGDTPRHLSNVST 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1744 GSLDNAHVPGGKNIKISQKINFRHNAKARVDHGAELIITQSPSSVSPRLSNVSSS 1803
QY 415 GSIDVDSPOLATLADDEVASLAKOGL 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1804 GSINLESPOLATLADDEVTAALAKOGL 1830

RESULT 13
A40115
microtubule-associated protein MAP2 - mouse
N:Alternate names: MAP2
C:Species: Mus musculus (house mouse)
C>Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 13-Aug-1999
C:Accession: A40115; S06467
R:Lewis, S.A.; Wang, D.; Cowan, N.J.
Science 242, 936-939, 1988
A:Title: Microtubule-associated protein MAP2 shares a microtubule binding motif with tau
A:Reference number: A40115; MUID:89043973
A:Accession: A40115
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1828 <LEW>
A:Cross-references: GB:M21041; NID:g199022; PIDN:AAA9490.1; PID:g199023
R:Mann, D.; Lewis, S.A.; Cowan, N.J.
Nucleic Acids Res. 16, 11369-11370, 1988
A:Title: Complete sequence of a cDNA encoding mouse MAP2.
A:Reference number: S06467; MUID:89083571
A:Accession: S06467
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-1828 <MAN>
A:Cross-references: GB:M21041; NID:g199022; PIDN:AAA9490.1; PID:g199023
C:Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C:Keywords: microtubule binding; tandem repeat
F:1670-1700/Domain: MAP2/tau repeat homology <MT1>
F:1701-1731/Domain: MAP2/tau repeat homology <MT2>
F:1732-1763/Domain: MAP2/tau repeat homology <MT3>

Query Match 31.4%; Score 719.5; DB 2; Length 1828;
Best Local Similarity 39.6%; Pred. No. 1.4e-29;
Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;

QY 44 KESPLQT-----PTDSESPGSETSDAKSTPAEDVTAPL-----VDEGAPKQAA 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1432 KEKFKTGGRISTPERKVAKEPSTVSRDEVRRKRAYKKAELAKKSEVOAHSPSRKLI 1491
QY 91 AQPTE-----IPEGTAEEAGIGDTPSLDEAGHTQARMYSKSDGTG----- 136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1492 LKPAIKYTRPHTLSCVKKRTTAASGDLAQAAPGAFKQADKTDG--IKSEKRSLSLP 1549
QY 137 -----SDKKAKAGADGKTIAIPRGAA-----PQOKQANATRIAPAKTPAPK 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1550 SSILPPRAGVSGDRENSFSLNSISARTRTSEPIRRACKSGSTPT--TPGSTAIRPG 1608
QY 181 TTPSSGEPKSGDSDSGYS--PGSPGTGSSKRTPSLPTPTREP--KVAVVRPPSP 236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1609 TTPS-----VSSRPTGTPGP--SYRPTGTPKSGILVPESEKVAIIRTPPKSP 1655
QY 237 SSAKSLQATAPVMPDLKAVKSKIGSTENLKHOPGGQVQIINKLDSLNVOSKSGSDN 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1656 ATPK-QLRNLNQLPDLKAVKSKIGSTENIKYOPKGGVQIVTKIDSH----- 1704
QY 297 IKHVPGGGVOIVYKPVDSLKSVTSKCSLGNIRHPPGGGQVEVSEKIDFKDROVQSKIGS 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1705 -----VTSKCGSLKNIRHPPGGGVYKLEESYKLDKEKAQAKV 1743
QY 357 LDNITHVPGGKNIETHKLTFRNNAKAKTIDGAEIYKSPVSGDTPRHLSNVSSS 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1744 LDNAHVPGGKNIKISQKINFRHNAKARVDHGAELIITQSPSSVSPRLSNVSSSGS 1803
QY 417 IDVDSPOLATLADDEVASLAKOGL 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1804 INLESPOLATLADDEVTAALAKOGL 1828

RESULT 14
S13507
microtubule-associated protein MAP2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 13-Aug-1999
C:Accession: S13507
R:Marchal, D.; Delapierre, D.; Dresse, A.
Arch. Int. Physiol. Biochim. 96, 231-236, 1988
A:Title: Cloning and partial sequencing of a new rat brain specific cDNA.
A:Reference number: S13507; MUID:89334524
A:Accession: S13507
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1825 <MAR>
A:Cross-references: EMBL:X54100; NID:g56624; PIDN:CAA38034.1; PID:g56625
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
C:Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C:Keywords: microtubule binding; tandem repeat
F:1667-1697/Domain: MAP2/tau repeat homology <MT1>
F:1698-1728/Domain: MAP2/tau repeat homology <MT2>
F:1729-1760/Domain: MAP2/tau repeat homology <MT3>

Query Match 31.3%; Score 717.5; DB 2; Length 1825;
Best Local Similarity 39.2%; Pred. No. 1.7e-29;
Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;

QY 44 KESPLQT-----PTDSESPGSETSDAKSTPAEDVTAPL-----VDEGAPKQAA 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1429 KEKFKTGGRISTPERKVAKEPSTVSRDEVRRKRAYKKAELAKKSEVOAHSPSRKLI 1488
QY 91 AQPTE-----IPEGTAEEAGIGDTPSLDEAGHTQARMYSKSDGTGSDDK 141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1489 LKPAIKYTRPHTLSCVKKRTTAASGDLAQAAPGAFKQADKTDG--IKSEKRSLSLP 1533
QY 142 AKGADGKTIAIPRGAA--GQK--QANATRIAPAKTPAPKTPSSGEPKSGDGRGY 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1534 TKSEKRSLSLPSSILPPRAGVSGDRENSFSLNSISARTRTS--EPIRACKSGT 1591
QY 198 SSPGSPG-----TSKRTPSLPTPT--REP-----KVAVVRPPSPS 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1592 STPTPGSTAITPPTGTPSSISRTPTGTPSTYRPTGTPKFGILVPESEKVAIIRTPPKS 1651
QY 236 PSSAKSLQATAPVMPDLKAVKSKIGSTENLKHOPGGQVQIINKLDSLNVOSKSGSDN 295
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1652 PATPK-QLRNLNQLPDLKAVKSKIGSTENIKYOPKGGVQIVTKIDSH----- 1701
QY 296 NIKHVPGGGVOIVYKPVDSLKSVTSKCSLGNIRHPPGGGQVEVSEKIDFKDROVQSKIG 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1702 -----VTSKCGSLKNIRHPPGGGVYKLEESYKLDKEKAQAKV 1739
QY 356 LDNITHVPGGKNIETHKLTFRNNAKAKTIDGAEIYKSPVSGDTPRHLSNVSSSG 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1740 SLDNAHVPGGKNIKISQKINFRHNAKARVDHGAELIITQSPSSVSPRLSNVSSSG 1799
QY 416 SIDVDSPOLATLADDEVASLAKOGL 441
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1800 SINLESPOLATLADDEVTAALAKOGL 1825

RESULT 15
QRHMT
microtubule-associated protein 2, splice form MAP-2b - human
N:Alternate names: MAP2
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1989 #sequence_revision 12-Apr-1996 #text_change 22-Jun-1999

```

C/Accession: I53693; A61085; P10024; S34131
R/Albala, J.S.; Kalcneva, N.; Shafit-Zagardo, B.
Gene 136, 377-378, 1993
A/Title: Characterization of the transcripts encoding two isoforms of human microtubule-
A/Reference number: I53693; MUID:94124038
A/Accession: I53693
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1824 <ALB>
A/Cross-references: EMBL:Z21958; GB:L12563; NID:g348216; PID:g348218
R/Dammerman, M.; Yen, S.H.; Shafit-Zagardo, B.
J. Neurosci. Res. 24, 487-495, 1989
A/Title: Sequence of a human MAP-2 region sharing epitopes with Alzheimer neurofibrillar
A/Reference number: A61085; MUID:90096190
A/Accession: A61085
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 77-645 <DAM>
R/Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Duffy, L.; Nave, R.L.
J. Neurochem. 51, 587-598, 1988
A/Title: Partial sequence of MAP2 in the region of a shared epitope with Alzheimer neuro
A/Reference number: P10024; MUID:88274407
A/Accession: P10024
A/Molecule type: mRNA
A/Residues: 489-1558 <KOS>
A/Cross-references: GB:M25668; NID:g187380; PIDN:AAA5952.1; PID:g187381
C/Comment: Microtubule-associated proteins are a complex group consisting of the high mo
they may stabilize the microtubules against depolymerization.
C/Genetics:
A/Gene: GDB:MAP2
A/Cross-references: GDB:118836; OMIM:157130
A/Map position: 2q34-q35
C/Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
C/Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F:1455-1463/Region: microtubule binding #status predicted
F:1666-1696/Domain: MAP2/tau repeat homology <MT1>
F:1697-1727/Domain: MAP2/tau repeat homology <MT2>
F:1728-1759/Domain: MAP2/tau repeat homology <MT3>
F:657,958,1064,1250,1436,1503/Binding site: phosphate (Thr) (covalent) #status predicted
F:697,817,829,1330,1417,1542,1551/Binding site: phosphate (Ser) (covalent) #status predi

Query Match 31.1%; Score 713.5; DB 1; Length 1824;
Best Local Similarity 36.5%; Pred. No. 2.7e-29;
Matches 189; Conservative 73; Mismatches 137; Indels 119; Gaps 18;

QY 2 AEPQEEFVMDHAGOPTYGLGDRKQ---GGYTHOEG-----DTDAGLKESPLQTP-P 51
DB 1348 ASPERE-EVALSEKTEY--DDYKDETTIDDSIMDADSLMVDQDDRSIMTEQLETIP 1404
QY 52 TEDGSEEPGSETSDAK-----STP---TAEDVTAPLYDE---GAPGKQA 89
DB 1405 KEKAEKEARSSLEKHKKEKFKTGKRGISTPERKVAKKKEPSTVSREYARKKAYKKA 1464
QY 90 AAOPTHELPEGTLEAGIGTLPSELEDAAGHTQARKVSKSKDGTGS-----DDKKAK 143
DB 1465 ELAKTEVOAHSFPRKFTL--KPAIKYTRPTHLSCVRKKTAAAGSESALAPSVFKQAKDK 1522
QY 144 GADGKTATPRGAP-----PGKG-----QANATRIPAKTP----- 176
DB 1523 VSDGVTSPFKRSSLPFRSSSLPFRKGYSGDRDENSFLNSISSAKRTTRSEPIRRAG 1582
QY 177 ---PAKTPPS---GEPKSGDRSGYSSPGSGTSGSRSTPSLPTTP---TRRP 223
DB 1583 KSGTSTPTPGSTAITPGTPSYSSR---TPGTPGP-TPRTPPTPGTPKSAIIVPSE 1637
QY 224 KKAIVRTPPKSPSSAKSLQTAIVPMDLKNVSKIGSTENLKHQGGGKVOIINKLD 283
DB 1638 KKAIVIRTPPKSPGLTPQLINQPLDLKNVSKIGSTDNIKYOPKGGVOIVTKKID 1697
QY 284 LSNVOSKSGSDNFKHPVGGGVQIVYKPVDSLKVTSGKSGSLGNIHKKPGGGGVSEK 343
DB 1698 LSH-----VTSKSGSLKNIRHRHPPGGGKVKIESVK 1726

QY 344 LDKRDVQSKIGSLDNTITHPGGNGKKIETHKLTRENAKAKTDHGAEIYKSPVYSGDT 403
DB 1727 LDKERKAQAQVGLDNAHHVPGGNGVKIDSKLTFREHAKARVDHGAEIITQSPGRSSVA 1786
QY 404 SPRLSNVSSGTGSDWVSPQATLADDEVASLAKQGL 441
DB 1787 SPRLSNVSSSGSINLLESPQATLADDEVTAALAKQGL 1824

Search completed: September 28, 2000, 20:00:11
Job time: 3721 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2000, 19:59:12 ; Search time 47.83 Seconds
(without alignments)
285,724 Million cell updates/sec

Title: US-09-142-613-1
Sequence: 1 MAPPROFEVMEHDAGDTR.....SPOLATLADVSASLAKOGL 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues
Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2262	98.6	441 1	TAU1_HUMAN
2	2011.5	87.6	448 1	TAU1_BOVIN
3	2003.5	87.3	432 1	TAU1_RAT
4	1512	65.9	341 1	TAU3_MOUSE
5	1508	65.7	364 1	TAU3_MOUSE
6	1493	65.1	402 1	TAU3_BOVIN
7	863.5	37.6	1861 1	MAP2_RAT
8	719.5	31.4	1828 1	MAP2_MOUSE
9	716	31.2	1827 1	MAP2_HUMAN
10	545	23.7	1152 1	MAP4_HUMAN
11	523.5	22.8	1125 1	MAP4_MOUSE
12	475	20.7	1072 1	MAP4_BOVIN
13	175.5	7.6	704 1	NP14_RAT
14	175.5	7.6	857 1	NP14_CHICK
15	163.5	7.1	825 1	ICP0_HSV2H
16	163.5	7.1	915 1	ICP0_HUMAN
17	161.5	7.0	670 1	VG50_HSV1
18	161.5	7.0	3924 1	NFM_RAT
19	161	7.0	3924 1	ANK2_HUMAN
20	160.5	7.0	1411 1	TCOF_HUMAN
21	160	7.0	1487 1	ICP4_HSV2H
22	158.5	6.9	1367 1	AMPH_YEAST
23	158	6.9	1487 1	ICP4_HSV2H
24	157	6.8	1164 1	BAG_STRAG
25	156.5	6.8	1906 1	KLMS_CHICK
26	155	6.8	699 1	VELG_HSV2H
27	155	6.8	1150 1	APMO_PIG
28	154.5	6.7	2805 1	MAPA_HUMAN
29	154	6.7	1446 1	IE18_PRIVA
30	154	6.7	1664 1	SLP1_CLODM
31	153.5	6.7	573 1	C114_MOUSE
32	152.5	6.6	1115 1	NKAL_MOUSE
33	152	6.6	1029 1	CA26_MOUSE

ALIGNMENTS

RESULT	1	STANDARD	PRT	441 AA.
TAU_HUMAN	1	1	1	1
TAU_HUMAN	1	1	1	1
AC	P10636; P18518; Q14799; Q15511;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	MICROTUBULE-ASSOCIATED PROTEIN TAU.			
GN	MAPT OR MTBT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 93041757.			
RA	Andreass A., Brown W.M., Kosik K.S.;			
RT	"Structure and novel exons of the human tau gene.";			
RL	Biochemistry 31:10626-10633(1992).			
RN	[2]			
RP	SEQUENCE OF 1-44 AND 103-441 FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 89251564.			
RA	Goedert M., Spillantini M.G., Potter M.C., Ulrich J., Crowther R.A.;			
RT	"Cloning and sequencing of the cDNA encoding a core protein of the			
RT	microtubule-associated protein tau containing four tandem repeats:			
RT	differential expression of tau protein mRNAs in human brain.";			
RL	EMBO J. 8:393-399(1989).			
RN	[3]			
RP	SEQUENCE OF 1-26 AND 306-441 FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 88234557.			
RA	Goedert M., Wischik C., Crowther R., Walker J., Klug A.;			
RT	"Cloning and sequencing of the cDNA encoding a core protein of the			
RT	paired helical filament of Alzheimer disease: identification as the			
RT	microtubule-associated protein tau.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).			
RN	[4]			
RP	SEQUENCE OF 1-26 AND 306-441 FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 90180482.			
RA	Lee G., Neve R.L., Kosik K.S.;			
RT	"The microtubule binding domain of tau protein.";			
RL	Neuron 2:1615-1624(1989).			
CC	-1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES			
CC	MICROTUBULES.			
CC	-1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE			
CC	PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.			
CC	-1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED			
CC	BY CAMP KINASE.			
CC	-1- DISEASE: TAU CONSTITUTES AT LEAST A PART OF THE PAIRED HELICAL			
CC	FILAMENT (PHF) CORE IN ALZHEIMER DISEASE.			
CC	-1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.			
CC	-1- DATABASE: NAME=HomoMolBase; NOTE=tau entry;			
CC	WWW=http://bioinformatics.weizmann.ac.il/homomolbase/entries/tau.htm.			

34	151.5	6.6	1020	1	BCA_STRAG	002192 streptococc
35	151.5	6.6	1020	1	NFM_HUMAN	P12036 homo sapien
36	151	6.6	1650	1	CA2B_MOUSE	Q64729 mus musculu
37	150.5	6.6	2468	1	MAPB_HUMAN	P46821 homo sapien
38	150	6.5	1210	1	AF4_HUMAN	P51825 homo sapien
39	149.5	6.5	1453	1	CA11_CHICK	P02457 gallus gall
40	149	6.5	783	1	FRB_HUMAN	O15117 homo sapien
41	149	6.5	1183	1	DRPL_RAT	P54258 rattus norv
42	149	6.5	1275	1	TRP_DROME	P19334 drosophila
43	148.5	6.5	339	1	CC06_CAEEL	P18831 caenorhabdi
44	148.5	6.5	817	1	VRP1_YEAST	P37370 saccharomyc
45	148	6.4	308	1	CC40_CAEEL	P34804 caenorhabdi

DR	EMBL:	AF027491;	AAC04279.1;	-	JOINED.
DR	EMBL:	AF047856;	AAC04279.1;	JOINED.	
DR	EMBL:	AF047857;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027482;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027493;	AAC04279.1;	JOINED.	
DR	EMBL:	AF047860;	AAC04279.1;	JOINED.	
DR	EMBL:	AF047862;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027494;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027495;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027496;	AAC04279.1;	JOINED.	
DR	EMBL:	AF047863;	AAC04279.1;	JOINED.	
DR	EMBL:	AF027491;	AAC04278.1;	-	JOINED.
DR	EMBL:	AF027492;	AAC04278.1;	JOINED.	
DR	EMBL:	AF027493;	AAC04278.1;	JOINED.	
DR	EMBL:	AF027496;	AAC04278.1;	JOINED.	
DR	EMBL:	AF047863;	AAC04278.1;	JOINED.	
DR	EMBL:	J033778;	CNA360615.1;	-	JOINED.
DR	EMBL:	X14474;	CNA32636.1;	-	
DR	PIR:	A30217;	QRHUT1.		
DR	PIR:	PN0001;	QRHTU2.		
DR	PIR:	S03796;	S03796.		
DR	MIM:	157140;	-		
DR	PFAM:	PF00418;	tubulin-binding; 4.		
DR	PROSITE,	PS00228;	TAU_MAP_1;	4.	
KW	Microtubules;	Repeat;	Alternative splicing;	phosphorylation.	
FT	REPEAT	244	274	TAU/MAP MOTIF.	
FT	REPEAT	275	305	TAU/MAP MOTIF.	
FT	REPEAT	306	336	TAU/MAP MOTIF.	
FT	REPEAT	337	368	TAU/MAP MOTIF.	
FT	DISEULFID	291	322	BY SIMILARITY.	
FT	VARSPLIC	45	102	MISSING (IN ISOFORM 1 AND ISOFORM 3).	
FT	VARSPLIC	275	305	MISSING (IN ISOFORM 2 AND ISOFORM 3).	
FT	VARSPLIC	1	44	MAEPREFEVEDAGTYGLADRKDDGGYTHQDEGDTDA GLK -> MLRALQGRK (IN FETAL ISOFORM).	
FT	VARSPIC	278	308	MISSING (IN FETAL ISOFORM).	
QO	SEQUENCE	441 AA:	45850 MW:	835A8706D847A8CC CRC64;	

[illegible]

```

RESULT      2
ID          TAU1_BOVIN
AC          P29172
DT          01-DEC-1992 (Rel. 24, Created)
DT          01-DEC-1992 (Rel. 24, Last sequence update)
DT          15-DEC-1998 (Rel. 37, Last annotation update)
DE          MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 1 AND 2.
GN          MAPT.
OS          Bos taurus (Bovine).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC          Bovidae; Bovinae; Bos.
NC          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE: 89261765.
RA          Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT          "Tau consists of a set of proteins with repeated C-terminal
RT          microtubule-binding domains and variable N-terminal domains.";
RL          Mol. Cell. Biol. 9:1381-1388(1989).
-1-         FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC          MICROTUBULES.
CC          -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC          PRODUCED BY ALTERNATIVE SPLICING.
CC          -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC          -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC          BY CAMP KINASE.
CC          -1- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
CC          -----
CC          THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on
CC          use by non-profit institutions as long as its content is in no way
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RL Science 239:285-288(1988).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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CC -----
DR EMBL: M18775; AAA40165.1; -.
DR PIR: B28820; B28820.
DR MGD: MGI:97180; MTAPT.
DR PFM: PFO0418; tubulin-binding; 3.
DR PROSITE: PS00229; TAU_MAP_1; 3.
DR Microtubules; Repeat; Alternative splicing.
FT REPEAT 175 205 TAU/MAP MOTIF.
FT REPEAT 206 236 TAU/MAP MOTIF.
FT REPEAT 237 268 TAU/MAP MOTIF.
SQ SEQUENCE 341 AA; 35714 MW; 478641931A5A4143 CRC64;

Query Match 65.9%; Score 1512; DB 1; Length 341;
Best Local Similarity 69.7%; Pred. No. 7.6e-66;
Matches 310; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

QY 1 MAEPROEFVEYEDHAGDQDTYGLGDRKDGQGYTM--HDSPTDAGLKEPSLQPTEDGSEE 58
DB 1 MADPROEFDLMEHDHAGD-----YLLDQDEGDMDHGLK----- 33
QY 59 PGSETSDAKSPTAEVTAFLVDEGAPGQAAAPHTPEIGTAEAGIGDTPLEDEA 118
DB 34 -----AEEAGIGDTPNOEDQA 49
QY 119 AGHTQAAMVSKSKDGTSGDDKAKAGADGKT--KATPRGAAPPGQAGQANATRIAPKTP 176
DB 50 AGHTQAQAVV--SKDRGTNDEKAKAGADGKTGAKIATPRGAAPGQAGTSMATRIAPKTP 107
QY 177 PAPTPPSGSGPPKSGRSGYSSPGSPGTPGSRKTPSLPTPTREPKKVAAYVTRTPKSP 236
DB 108 PSPKTPPSGSGPPKSGRSGYSSPGSPGTPGSRKTPSLPTPTREPKKVAAYVTRTPKSP 167
QY 237 SSAKSRLOTAPVPMPELDKLVKSKIGSTENLKHOPGCGKQVQIINKKLDLSNVQSKGSKDN 296
DB 168 SAKSRLOTAPVPMPELDKLVKSKIGSTENLKHOPGCGK----- 205
QY 297 IKHVPGGGVOIYKPVULSKVTSKCGSLGNHHRKPGGGQVEYKSEKLDKDRVQSKGS 356
DB 206 -----VOIYKPVULSKVTSKCGSLGNHHRKPGGGQVEYKSEKLDKDRVQSKGS 256
QY 357 LDNITHVGGGNNKIETKLTFRENAKAKTDHGAETIYKSPVSGDTSPRHLSNVSGTGS 416
DB 257 LDNITHVGGGNNKIETKLTFRENAKAKTDHGAETIYKSPVSGDTSPRHLSNVSGTGS 316
QY 417 IDWVDSPOLATLADSVASLAKOGL 441
DB 317 IDWVDSPOLATLADSVASLAKOGL 341

RESULT 5
TAU2_MOUSE STANDARD; PRT; 364 AA.
ID TAU2_MOUSE
AC P10638;
DT 01-JUL-1989 (Rel. 11, Created)
DI 01-JUL-1989 (Rel. 11, Last sequence update)

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DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TAZ2).
GN MAPT OR MTAPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 88099510.
RA Lee G., Cowan N.J., Kirschner M.;
RT "The primary structure and heterogeneity of tau protein from mouse
RL brain."
RL Science 239:285-288(1988).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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CC -----
DR EMBL: M18776; AAA40166.1; -.
DR PIR: A28820; A28820.
DR MGD: MGI:97180; MTAPT.
DR PFM: PFO0418; tubulin-binding; 3.
DR PROSITE: PS00229; TAU_MAP_1; 3.
DR Microtubules; Repeat; Alternative splicing.
FT REPEAT 175 205 TAU/MAP MOTIF.
FT REPEAT 206 236 TAU/MAP MOTIF.
FT REPEAT 237 268 TAU/MAP MOTIF.
SQ SEQUENCE 364 AA; 38199 MW; DICAB2EF89CDD7C0 CRC64;

Query Match 65.7%; Score 1508; DB 1; Length 364;
Best Local Similarity 69.6%; Pred. No. 1.3e-65;
Matches 309; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

QY 1 MAEPROEFVEYEDHAGDQDTYGLGDRKDGQGYTM--HDSPTDAGLKEPSLQPTEDGSEE 58
DB 1 MADPROEFDLMEHDHAGD-----YLLDQDEGDMDHGLK----- 33
QY 59 PGSETSDAKSPTAEVTAFLVDEGAPGQAAAPHTPEIGTAEAGIGDTPLEDEA 118
DB 34 -----AEEAGIGDTPNOEDQA 49
QY 119 AGHTQAAMVSKSKDGTSGDDKAKAGADGKT--KATPRGAAPPGQAGQANATRIAPKTP 176
DB 50 AGHTQAQAVV--SKDRGTNDEKAKAGADGKTGAKIATPRGAAPGQAGTSMATRIAPKTP 107
QY 177 PAPTPPSGSGPPKSGRSGYSSPGSPGTPGSRKTPSLPTPTREPKKVAAYVTRTPKSP 236
DB 108 PSPKTPPSGSGPPKSGRSGYSSPGSPGTPGSRKTPSLPTPTREPKKVAAYVTRTPKSP 167
QY 237 SSAKSRLOTAPVPMPELDKLVKSKIGSTENLKHOPGCGKQVQIINKKLDLSNVQSKGSKDN 296
DB 168 SAKSRLOTAPVPMPELDKLVKSKIGSTENLKHOPGCGK----- 205
QY 297 IKHVPGGGVOIYKPVULSKVTSKCGSLGNHHRKPGGGQVEYKSEKLDKDRVQSKGS 356
DB 206 -----VOIYKPVULSKVTSKCGSLGNHHRKPGGGQVEYKSEKLDKDRVQSKGS 256
QY 357 LDNITHVGGGNNKIETKLTFRENAKAKTDHGAETIYKSPVSGDTSPRHLSNVSGTGS 416
DB 257 LDNITHVGGGNNKIETKLTFRENAKAKTDHGAETIYKSPVSGDTSPRHLSNVSGTGS 316

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DB 257 LDNTHVGGGKKIETHTKLTFRNNAKAKTDHGAETIVKSPVSGDTSFRHLNVSSTGS 316

QY 417 IDWDSPOLATLADDEVASASLAKOG 440
 |||||
 DB 317 IDWDSPOLATLADDEVASASLAKOG 340

RESULT 6
 TAU3_BOVIN
 ID TAU3_BOVIN STANDARD; PRT; 402 AA.
 AC P29173:
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 3, 4, AND 5.
 GN MAPT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89361765.
 RA Hummler A., Drechsel D., Kirschner M.W., Martin D.M. Jr.;
 RT "tau consists of a set of proteins with repeated C-terminal
 RT microtubule-binding domains and variable N-terminal domains";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
 CC -1- PFM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
 CC BY CAMP KINASE.
 CC -1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
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 CC
 CC EMBL: M26158; AAA30771.1; -
 DR PIR: B31939; ORBOT2.
 DR PFM: PF00418; tubulin-binding; 4.
 DR PROSITE: PS00229; TAU_MAP_1; 4.
 KW Microtubules; Repeat; Alternative splicing.
 FT REPEAT 205 235 TAU/MAP MOTIF.
 FT REPEAT 236 266 TAU/MAP MOTIF.
 FT REPEAT 267 297 TAU/MAP MOTIF.
 FT REPEAT 298 329 TAU/MAP MOTIF.
 FT VARSPEC 1 100 MISSING (IN ISOFORM 4).
 FT VARSPEC 235 296 MISSING (IN ISOFORM 5).
 FT VARSPEC 402 AA; 42232 MW; A7FCED47A04D7340 CRC64;
 SQ

Query Match 65.1%; Score 1493; DB 1; Length 402;
 Best Local Similarity 79.7%; Pred. No. 7.2e-65;
 Matches 303; Conservative 14; Mismatches 29; Indels 34; Gaps 6;

QY 64 SDASTPTAEVTAPLVDEGAPGKAAQAQPTETPEGTAEAGIGTPSLEDBAAGHT 123
 |||||
 DB 55 SPKPTGSSD---PLIKPSP-----AVCPSSSSSK-----HVS 87

QY 124 QARNVSKSKDGTSGDDKAKGADCK--TKATPPGAAPPGQKGAATRIAPAKTPPAKT 181
 |||||
 DB 88 S---VTPRTGSGAKEMKVGADGKPGKRIATPGAAPPGQKGAATRIAPAKTPPAKT 144

QY 182 PPSGGEPPKSDRBGYSPPSGSPGTGSKSRPSLPTPTTRPKAVAYVTRTPKSPSAKS 241
 |||||
 DB 145 -SP--GESGKSGDRSGYSSPGSPGTGSKSRPSLPTPTTRPKAVAYVTRTPKSPSAKS 202

QY 242 RLQATPVPMDLKNVSKISSTENLKHQPGGKVOIINKKLDSNVOSKCGSKDNITHVP 301
 |||||
 DB 203 RLQAAPGPMPLDKNVKSKISTENLKHQPGGKVOIINKKLDSNVOSKCGSKDNITHVP 262

QY 302 GGGSVQIVYKRPVLSKTSKCGSLGNHHKPPGGQVYVSEKLDKRVOSKIGSLDNIT 361
 |||||
 DB 263 GGGSVQIVYKRPVLSKTSKCGSLGNHHKPPGGQVYVSEKLDKRVOSKIGSLDNIT 322

QY 362 HVPGGKKIETHTKLTFRNNAKAKTDHGAETIVKSPVSGDTSFRHLNVSSTGSIDMD 421
 |||||
 DB 323 HVPGGKKIETHTKLTFRNNAKAKTDHGAETIVKSPVSGDTSFRHLNVSSTGSIDMD 382

QY 422 SPOLATLADDEVASASLAKOG 441
 |||||
 DB 383 SPOLATLADDEVASASLAKOG 402

RESULT 7
 MAP2_RAT
 ID MAP2_RAT STANDARD; PRT; 1861 AA.
 AC P15146;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
 GN MAP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE: 90251471.
 RA Kindler S., Schwabe B., Schulz B., Garner C.C.;
 RT "Complete cDNA sequence encoding rat high and low molecular weight
 RT MAP2";
 RL Nucleic Acids Res. 18:2822-2822(1990).
 RN [2]
 RP SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE: 91060576.
 RA Kindler S., Schulz B., Goedert M., Garner C.C.;
 RT "Molecular structure of microtubule-associated protein 2b and 2c from
 RT rat brain";
 RL J. Biol. Chem. 265:19679-19684(1990).
 RN [3]
 RP SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
 RX MEDLINE: 90221819.
 RA Doll T., Papadimitrakopoulou A., Matus A.;
 RT "Nucleotide and amino acid sequences of embryonic rat MAP2c";
 RL Nucleic Acids Res. 18:361-361(1990).
 RN [4]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE: 89361519.
 RA Papadimitrakopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
 RT "Embryonic MAP2 lacks the cross-linking sidearm sequences and
 RT dendritic targeting signal of adult MAP2";
 RL Nature 340:650-652(1989).
 RN [5]
 RP SEQUENCE OF 1695-1725 FROM N.A.
 RX MEDLINE: 94110302.
 RA Doll T., Melchener M., Riederer B.M., Honegger P., Matus A.;
 RT "An isoform of microtubule-associated protein 2 (MAP2) containing
 RT four repeats of the tubulin-binding motif";
 RL J. Cell Sci. 106:633-640(1993).
 CC -1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
 CC STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
 CC SEEM TO HAVE A STRENGTHENING EFFECT ON MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
 CC FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
 CC -1- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN


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CC DEVELOPMENT AND UNTIL POSTANTAL DAY 10. MAP2B IS EXPRESSED
CC THROUGHOUT BRAIN DEVELOPMENT.
CC -1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
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CC -----
DR EMBL: X51842; CA36135.1; -
DR EMBL: X17682; CA35667.1; -
DR EMBL: X71487; CA50588.1; -
DR PIR: S07887; S07887.
DR PIR: S10003; S10003.
DR PIR: A37981; A37981.
DR PIR: P000418; tubulin-binding; 4.
DR PROSITE: PS00229; TAU_MAP_1; 3.
KW Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT DOMAIN 1454 1474 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1664 1694 TAU/MAP MOTIF.
FT REPEAT 1695 1725 TAU/MAP MOTIF.
FT REPEAT 1726 1756 TAU/MAP MOTIF.
FT REPEAT 1757 1788 TAU/MAP MOTIF.
FT VARSPPLIC 152 1514 MISSING (IN ISOFORM MAP2C).
FT VARSPPLIC 1695 1725 MISSING (IN ISOFORM WITH 3 TAU/MAP
FT REPEATS).
SQ SEQUENCE 1861 AA; 202409 MW; 42DCFF116D21EF54E CRC64;

Query Match 37.6%; Score 863.5; DB 1; Length 1861;
Best Local Similarity 44.3%; Pred. No. 2,7e-34;
Matches 198; Conservative 67; Mismatches 115; Indels 67; Gaps 12;

QY 44 KESPLQT-----PTEDGSEPPGSETSDAKSTPTAEDVTAPLVDEG-----APCKQA 89
DB 1433 KEKPFKGRGRISTPERREVAKEPSTVSDEVRKRAVYKKAELAKESEVOAHSPPKRL 1492
QY 90 AAOHTE-----IPEGTAEAGIGDTPSLDEAGHYTAQARVSKSDGTGSDK 140
DB 1493 ILKAIKYTRTHLSCKVKKRTTATGSESAQAPSAFKQAKDKVT-----DG 1537
QY 141 KAKGADCKTKIATPRGAAP--GQKG--QANATRIAPKTPPPSGEPKSGDPSRG 196
DB 1538 ITKPEKRSLSIPRPSSTILPRRGVSGDRENSFSLNSSISSARRTTR--EPIRRAGSG 1595
QY 197 YSSFGSGG---TPGS---RSRTPSLPTPT--REP-----KKVAVVTRPPK 234
DB 1596 TSPETPGSAITPGTPPSYSSRTPTGTPSYPTPTGPKSGILVPESEKVAIIRTPPK 1655
QY 235 SPSSAKRLQATAPVPMDLKLVKSKIGSTENLKHQPGGQVQIINKKLDSLNVQSKGSK 294
DB 1656 SPAPRK-QLRLINPLPDLKLVKSKIGSTDNKIKYQPGGQVRIILKKDKFVSQSGSKG 1714
QY 295 DNKIHVGGGVSQIVYKRPVDLSKVTSGSLGNITHHKPPGGGVGVSEKDLDFKRVOSKI 354
DB 1715 DNKIHSAAGGVQIVTKKIDLSHVTSGSKGLNIRHRPGGGRVAVIESKIDDFKKAQAKV 1774
QY 355 GSLDNHVVHGGGKKEIETHKILFRENAKAKTDHGAELIYKSPVYSGDTSRHLNSVST 414
DB 1775 GSLDNHVVHGGGKKEIDSKLNFRENAKAKAVDHAELITQSPERSRVSASPRRLSNVSS 1834
QY 415 GSIDMVDSQPLATLADSVASLAKOGL 441
DB 1835 GSINLLESPQPLATLADSVTALAAGL 1861

RESULT 8
MAP2_MOUSE STANDARD; PRT; 1828 AA.
AC P20357;

DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN 2.
GN MAP2 OR TMAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89083571.
RA Wang D., Lewis S.A., Cowan N.J.;
RT "Complete sequence of a cDNA encoding mouse MAP2."
RL Nucleic Acids Res. 16:11369-11370(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89043973.
RA Lewis S.A., Wang D., Cowan N.J.;
RT "Microtubule-associated protein MAP2 shares a microtubule binding
RT motif with tau protein."
RL Science 242:936-939(1988).
CC -1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC STABILIZE THE MICROTUBULES AGAINST DOPOLYMERIZATION. THEY ALSO
CC SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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CC -----
DR EMBL: M21041; AAA39490.1; -
DR PIR: S06467; S06467.
DR PIR: A40115; A40115.
DR MGD; MGI:97175; MTA2.
DR PIR: P000418; tubulin-binding; 3.
DR PROSITE: PS00229; TAU_MAP_1; 2.
KW Microtubules; Repeat; Calmodulin-binding.
FT DOMAIN 1452 1472 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1662 1692 TAU/MAP MOTIF.
FT REPEAT 1693 1723 TAU/MAP MOTIF.
FT REPEAT 1724 1755 TAU/MAP MOTIF.
SQ SEQUENCE 1828 AA; 198980 MW; 200BC59E3605386A CRC64;

Query Match 31.4%; Score 719.5; DB 1; Length 1828;
Best Local Similarity 39.6%; Pred. No. 1.8e-27;
Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;

QY 44 KESPLQT-----PTEDGSEPPGSETSDAKSTPTAEDVTAPL-----YDEGAPCKQA 90
DB 1432 KEKPFKGRGRISTPERKAKKEPSTVSDEVRKRAVYKKAELAKSEVOAHSPPKRL 1491
QY 91 AOHTE-----IPEGTAEAGIGDTPSLDEAGHYTAQARVSKSDGTG----- 136
DB 1492 LKAIKYTRTHLSCKVKKRTTATGSAQAPSAFKQAKKYVDG--ISSPKRSLSLPP 1549
QY 137 -----SDKKAAGDKTKIATPRGA-----PPGQKQANATRIAPKTPPAK 180
DB 1550 SSILPRRGVSGDRENSFSLNSSISSARRTTSEPIRRAKSGSTPT--TPGSTAITPG 1608
QY 181 TPSSGSEPPRSGDPSYSS--PGSPGTGSRSTPSPPTPPREP--KKVAVVTRPPKSP 236
DB 1609 TPSS-----YSSRTPGTPTPT--SYPTPTGTPPSGILVPESEKVAIIRTPPKSP 1655
QY 237 SSASRLQATAPVPMDLKLVKSKIGSTENLKHQPGGQVQIINKKLDSLNVQSKGSKDN 296
DB 1656 ATPK-QLRLINPLPDLKLVKSKIGSTDNKIKYQPGGQVQIVTKKIDLSH----- 1704
QY 297 IKHVPGGGVSQIVYKRPVDLSKVTSGSLGNITHHKPPGGGVGVSEKDLDFKRVVSKIGS 356

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DB 1705 -----VTSKCGSLKNIHRPGGGRVATIESVKLDFKKAQAKVGS 1743
QY 357 LDNITHVPGGKNIETHTKLTFRNNAKATDGAELIVYSPVSGDTPSRHLSNVSTGS 416
DB 1744 LDNAHVPGGKNIETHTKLTFRNNAKATDGAELIVYSPVSGDTPSRHLSNVSTGS 1803
QY 417 IDWDSPQATLADSVASLAKOGL 441
DB 1804 INLESPLATLADVTALAKOGL 1828

RESULT 9
MAP2_HUMAN STANDARD: PRT; 1827 AA.
ID MAP2_HUMAN 099976; 099975;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
GN MAP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RA PRICE R.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-BRAIN;
RA MEDLINE; 94124038.
RA Alcala J.S., Kalcheva N., Shafit-Zagardo B.;
RT "Characterization of the transcripts encoding two isoforms of human
RL microtubule-associated protein-2 (MAP-2).";
RL Gene 136:377-378(1993).
RN [3]
RP SEQUENCE OF 493-1562 FROM N.A.
RA MEDLINE; 88274407.
RA Kosik K.S., Orecchio L.D., Bakalis S., Duffy L., Neve R.L.;
RT "Partial sequence of MAP2 in the region of a shared epitope with
RL Alzheimer neurofibrillary tangles."
RL J. Neurochem. 51:587-598(1988).
CC -1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
CC STABILIZE THE MICROTUBULES AGAINST DEPOLYMERIZATION. THEY ALSO
CC SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
CC ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
CC FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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CC -----
DR EMBL; U01828; AAA03354.1; -
DR EMBL; U89330; AAB48098.1; -
DR EMBL; U89329; AAB48097.1; -
DR EMBL; M25668; AAA59552.1; -
DR PIR; PLO024; ORH0MT.
DR MIM; 157130; -
DR PFM; PF00418; tubulin-binding; 3.
DR PROSITE; PS00229; TAU_MAP_1; 2.
KM Microtubules; Repeat; Alternative splicing; Calmodulin-binding.
FT DOMAIN 1447 1467 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1661 1691 TAU/MAP MOTIF.
FT REPEAT 1692 1722 TAU/MAP MOTIF.
FT REPEAT 1723 1754 TAU/MAP MOTIF.
FT VARSPLC 152 1507 MISSING (IN ISOFORM MAP2C).

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FT CONFLICT 9 9 A -> G (IN REF. 2).
FT CONFLICT 37 37 R -> A (IN REF. 2).
FT CONFLICT 108 108 A -> G (IN REF. 2).
FT CONFLICT 152 155 MISSING (IN REF. 2).
FT CONFLICT 187 187 S -> K (IN REF. 2).
FT CONFLICT 1655 1655 A -> GL (IN REF. 2).
FT CONFLICT 1736 1736 V -> A (IN REF. 2).
SQ SEQUENCE 1827 AA; 199610 MW; BAC36D0030F5F455 CRC64;

Query Match 31.2%; Score 716; DB 1; Length 1827;
Best Local Similarity 36.9%; Pred. No. 2,7e-27;
Matches 191; Conservative 75; Mismatches 132; Indels 120; Gaps 19;

QY 2 AEPQEFVEMDHAGQDTYGLDRKQ---GGYTHQHG-----DTDAIKESPLOQ-P 51
DB 1352 ASPERE-EVALSEKTEY---DYKDETIDSDIMADSLWVDQDDRSIMTEQLTIP 1408
QY 52 TEDGSEEGSETSDAK-----STP-----TAEDVTAPLVE-----GAPGQA 89
DB 1409 KEKAKERARRSLEKHKREKPFKGTGRGISTPERKAKKEPTSVSRDEVRKRAVYKA 1468
QY 90 AAQPIETPEGTAEAGIDGTPSLDEPAAGVTOARVSKNDGTG-----DGRKAK 143
DB 1469 ELAKTEVQASHPSKFTL--KPAIKITRPTHLSCVKKRTTAGGESLAASVFRQAKD 1526
QY 144 GADGRTKIATPRGAP-----PGQG-----QANATRIPAKTP----- 176
DB 1527 VSDGVTKSPKRSILPRSSILPRGVSGRDENSEFSLNMISSABRTTRSEPIRAG 1586
QY 177 ----PAKTPRSS-----GEPKSGDRSGSYSPSGGTGSRPSLTTP-----TEEP 223
DB 1587 KSGISTPTPTSTALPTPTPSYSR---TPGTPGP-STPRPTPTGTAKSALVPS 1641
QY 224 KKVAVRTPRPPSPSSAKRLOTAPVMPDLKNVKSIGSTENLKHQPGGKVOIINKLD 283
DB 1642 KKVATIRTPPKSPATPK-QLILNPDLPLKNVKSIGSTENIKYQPGGVOIYTKKID 1700
QY 284 LSNVSKGSKNDIKHVPGGGSGVOIVKPVDSLKVTSGKSLGINHKPGGGQVEKSEK 343
DB 1701 LSH-----VTSKCGSLKNIHRPGGGRVATIESVK 1729
QY 344 LDFKRVOSKIGSLDNTITHVPGGKNIETHTKLTFRNNAKATDGAELIVYSPVSGDT 403
DB 1730 LDFKRVQAKGSLDNAHVPGGKNIETHTKLTFRNNAKATDGAELIVYSPVSGDT 1789
QY 404 SPRHLSNVSTGSDWDSPQATLADSVASLAKOGL 441
DB 1790 SPRHLSNVSSGSLVLESPLATLADVTALAKOGL 1827

RESULT 10
MAP4_HUMAN STANDARD: PRT; 1152 AA.
ID MAP4_HUMAN 099976; 099975;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN 4.
GN MAP4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RA PRICE R.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA MEDLINE; 92042100.
RA West R.R., Tendler K.M., Olmsted J.B.;
RT "A model for microtubule-associated protein 4 structure. Domains
RL defined by comparisons of human, mouse, and bovine sequences."
RL J. Biol. Chem. 266:21886-21896(1991).
RN [2]
RP SEQUENCE OF 102-1152 FROM N.A.
RC TISSUE-BRAIN;

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RX MEDLINE: 91277031.
RA Chapin S.J., Bullinsk J.C.;
RT "Non-neuronal 210 x 10(3) Mr microtubule-associated protein (MAP4)
RT contains a domain homologous to the microtubule-binding domains of
RT neuronal MAP2 and tau."
RL J. Cell Sci. 98:27-36(1991).
CC -1- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES
CC MICROTUBULE ASSEMBLY.
CC -1- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS
CC NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE
CC ASSEMBLY.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64571; AAA59553.1; -.
DR PIR: A33183; A33183.
DR PIR: A41206; A41206.
DR MIM: 157132; -.
DR PFAM: PF00418; tubulin-binding; 4.
DR PROSITE: PS00229; TAU_MAP_1; 4.
KM Microtubules; Repeat; Phosphorylation; Alternative splicing.
FT DOMAIN 248 545 17 X 14 AA TANDEM REPEATS.
FT REPEAT 248 261 1.
FT REPEAT 262 275 2.
FT REPEAT 274 289 3.
FT REPEAT 290 303 4.
FT REPEAT 304 317 5.
FT REPEAT 318 331 6.
FT REPEAT 332 345 7.
FT REPEAT 346 351 8 (INCOMPLETE).
FT REPEAT 352 377 26 RESIDUES 1.
FT REPEAT 378 403 26 RESIDUES 2.
FT REPEAT 408 421 9.
FT REPEAT 422 433 10.
FT REPEAT 434 447 11.
FT REPEAT 448 461 12.
FT REPEAT 462 475 13.
FT REPEAT 476 489 14.
FT REPEAT 490 503 15.
FT REPEAT 504 517 16.
FT REPEAT 532 545 17.
FT REPEAT 923 953 TAU/MAP MOTIF.
FT REPEAT 992 1022 TAU/MAP MOTIF.
FT REPEAT 1023 1053 TAU/MAP MOTIF.
SO SEQUENCE 1152 AA; 121180 MW; 0B6CF0CF926B558F CRC64;

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QY 196 GYSSPSPGTPRSKRTPTLPTPT--EPKVAVWTP-----PKSPSSAK---- 240
DQ 857 DLSRKRSTSSMKKTTLTSTAPAGVPSRVATMPSPSPSTPRIDKKPTAKRPSST 916
QY 241 ---SLQTAVPMDLKNVSKSTGSTEENLKHPG----- 272
DQ 917 TPRLSRLAT-NTSAPDLKNVSKVSTENIKHPGGGRAYEKTEAATTRKPSNAVY 975
QY 273 -----GKYOINKKIDLSNVOSKSGSKXNKHVPPGGVQVLYKPYDLSKY 318
DQ 976 KTAEPASAGKOPAGKVOIVSKVSYSHIOSKSKXNKHVPPGGVQVQONKKVDISKY 1035
QY 319 TSKGSLGNIHRRKGGEVEYSEKIDFKDVRVOSKIGSLDNITHVPGGKMKIETHKLT 378
DQ 1036 SSKGSKRNINHKRGGDYKIESOKLNFKEAKVAGSLDNVGLTPAG----- 1084
QY 379 RBNKAKTDBAELVYKSPVVSQDTPRHLSNVSTGSDIDVDSPOLATLADSVASLAK 438
DQ 1085 ---AVKTEGGGS---EAPLCPPGPAG-----EPPAISFAPEAGAPTSA 1122
QY 439 QGL 441
DQ 1123 SGL 1125

```

RESULT 11

MAP4_MOUSE

MAP4_MOUSE STANDARD; PRT; 1125 AA.

AC P27546;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE MICROTUBULE-ASSOCIATED PROTEIN 4.

GN MAP4 OR MTAP4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 92042100.

RA West R.R., Tenbarge K.M., Olmsted J.B.;

RT "A model for microtubule-associated protein 4 structure. Domains defined by comparisons of human, mouse, and bovine sequences.";

RL J. Biol. Chem. 266:21886-21896(1991).

CC -1- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES MICROTUBULE ASSEMBLY.

CC -1- TISSUE SPECIFICITY: TESTIS, STRIATED AND CARDIAC MUSCLE.

CC -1- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE ASSEMBLY.

CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.

CC -----

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CC -----

DR EMBL: M72414; AAA16372.1; -.
DR PIR: B41306; B41306.
DR MIM: MGI:97178; MTAP4.
DR PFAM: PF00418; tubulin-binding; 4.
DR PROSITE: PS00229; TAU_MAP_1; 3.
KM Microtubules; Repeat; Phosphorylation.
FT REPEAT 896 926 TAU/MAP MOTIF.
FT REPEAT 965 995 TAU/MAP MOTIF.
FT REPEAT 996 1026 TAU/MAP MOTIF.
SO SEQUENCE 1125 AA; 117675 MW; 73047432A325A1D CRC64;

Query Match 22.8%; Score 523.5; DB 1; Length 1125;
 Best Local Similarity 33.9%; Pred. No. 2.3e-16;
 Matches 149; Conservative 51; Mismatches 128; Indels 111; Gaps 14;

44 KESPIQPTDESEPESESTSDAKSTPTAEVTAADLVDEGAGKQAAAP-HTEIPEGTT 102
 625 KETPGQPEPEPSGVSRQEAAGAAGVGNDDITPPNKEPPSPKKAKPLATTPAKNS 684
 103 ABEA-----GIGDTP---SLEDEAGHTQAMNYSKSDGT--GSD 139
 685 TSKAKTQPTSLKPAPPTSGGLNKKPMSLAGSVPAAPHKRPAATATARPSTLPADY 744
 140 K-----KAKGAGKTKIATPRG--AAPPGK-----GQANARIRAKT-P 176
 745 KRPPTTEAAVAKRTSPSKSSAPALPKPPKPTPVSKATSPSTVSTGSSSPATLTP 804
 177 PAPPTPPSSGEP-----PKSGDRSGYSSPGSPGSRKTPSLPPTP-----TR--- 221
 805 KRPSTIKTGKRAVYKRMATAKASADLSKSKTSSSVKRNRTTPGAAPRACMTSTRVKP 864
 222 --EPKAVAVVTRTPKSPSSAK-----SRQTAAPVPPMDIKNYSKIGSTENIKHOPG 271
 865 MSAPRSRGALSVDKKPTSTKSSAPRVSLATP-VSAPDLKSVRSKVGSTENIKHOPG 923
 272 G-----GKVOIINKKIDLSNNVSKGCS 293
 924 GGRAYEKKTEATAGKREPNAVTKAAGSISAOCPKPAKVOIVSKVSYSHISKVCS 983
 294 KNIKHVPGGGSVQIVYKPVDSLTKYTSKGLNHHKRGGOVEKSEKIDPKRVOSK 353
 984 KNIKHVPGGGSVQIVYKPVDSLTKYTSKGLNHHKRGGOVEKSEKIDPKRVOSK 1043
 354 IGSIDNTHVPGGSKKIE 372
 1044 VGSIDNVGHFPAGAVKTE 1062

RESULT 12
 MAP4_BOVIN STANDARD; PRT: 1072 AA.

AC P36225;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN 4 (MICROTUBULE-ASSOCIATED PROTEIN-U) (MAP-U).
 GN MAP4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 90338002.
 RA Aizawa H., Emori Y., Murofushi H., Kawasaki H., Sakai H., Suzuki K.;
 RT "Molecular cloning of a ubiquitously distributed microtubule-associated protein with Mr 190,000.";
 RL J. Biol. Chem. 265:13849-13855(1990).
 RN [2]
 RP DOMAINS.
 RX MEDLINE: 91236765.
 RA Aizawa H., Emori Y., Mori A., Murofushi H., Sakai H., Suzuki K.;
 RT "Functional analyses of the domain structure of microtubule-associated protein-4 (MAP-U).";
 RL J. Biol. Chem. 266:9841-9846(1991).
 CC -1- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES MICROTUBULE ASSEMBLY.
 CC -1- TISSUE SPECIFICITY: IS DISTRIBUTED UBQUITOUSLY AMONG ALL TISSUES BUT AMOUNTS ARE LOWER IN CEREBELLUM AND LIVER.
 CC -1- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE ASSEMBLY.

CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
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 CC EMBL: D90149; BA14179.1; .
 CC PIR: A37127.
 DR PIR: A37127; tubulin-binding; 3.
 DR PROSITE: PS00229; TAU_MAP_1; 3.
 KW Microtubules; Repeat; Phosphorylation.
 FT DOMAIN 244 530
 FT REPEAT 244 530 19 x 14 AA TANDEN REPEATS.
 FT REPEAT 258 271 1.
 FT REPEAT 272 285 2.
 FT REPEAT 286 299 3.
 FT REPEAT 300 313 4.
 FT REPEAT 314 327 5.
 FT REPEAT 328 341 6.
 FT REPEAT 342 355 7.
 FT REPEAT 384 391 8.
 FT REPEAT 392 405 9 (INCOMPLETE).
 FT REPEAT 406 417 10.
 FT REPEAT 418 431 11.
 FT REPEAT 432 445 12.
 FT REPEAT 446 460 13.
 FT REPEAT 461 474 14.
 FT REPEAT 475 488 15.
 FT REPEAT 489 502 16.
 FT REPEAT 503 516 17.
 FT REPEAT 517 530 18.
 FT REPEAT 907 937 19.
 FT REPEAT 938 968 TAU/MAP MOTIF.
 FT REPEAT 969 1000 TAU/MAP MOTIF.
 SO SEQUENCE 1072 AA; 111914 MW; E8C17A730989F0D2 CRC64;

Query Match 20.7%; Score 475; DB 1; Length 1072;
 Best Local Similarity 31.7%; Pred. No. 4.4e-16;
 Matches 145; Conservative 53; Mismatches 132; Indels 128; Gaps 20;

32 TMHOGDIDAGLKESP-----LQTPEDGS-----EEPGSESDAKSTPTAEV 75
 558 SLODEGQSAVPLMTSPFAVYVAMGQKHSPTDESDVLEBEQKKSSQTSLEPSETSG--V 615
 76 TAPLVDEGAP-----GQAAAQPTTEIPEGTTAEAGIGDTPSLEDEAGHTQAMNYSK 130
 616 AKP--EEGPPRGSVSGNDITAPNKEKLPSPKKTKPLATQPKTSKAKTQPTSLPK 673
 131 SKDGT---GSDDKAKAGDKTKITATPRGAAPPGOKGQANA--TRIPAK-TTPAP---K 180
 674 QTAPTLGSKNKKPMSLAGSVP-----AAPKRPAAATJRPSTLPSKDKTPKPVAEAK 727
 181 TP-----SSGEPPKSGDRSGYSSPGSGT-----PGSRSTPSLPPTP--PT----- 220
 728 IPEKRVSPSKASAPAYKPGSGSTQAVPKAPATATLASPGSTSNLSPLDKRPTAITE 787
 221 --REPKAVAVVTRP---PKS-----PSSAKSRLQ---TAPVP--- 249
 788 GKPEIKKMAKSPADLSRPSSTTSVKKSTVPGAPAPAGAPARRAPRPTPPRPGT 847
 250 -----MPDKNYSKIGSTENIKHOPGGGKVOIINKKL 282
 848 PPVDDKPTPAKPTSSAPRLGVAAANASAPADLKNVRSKVGSTENIKHOPGGGKRAV-VEKKT 906
 283 DLS-----NVOSKSGSKDNIKHVPGGGSVQIVYKPVDSLTKYTSKGLNHHKPGG 334
 907 EAAAPARKPEPNAVTKAAGPIGNMOKPPTGKVOIONKKNVDSKYSKCGSKGSKANIKHKGPG 966

OY 335 GOVEYKSEKIDFKRVOSKISLNDITHVPGGKNKIE 372
 DB 967 GVKIESOKINFKERAKVAGSLDNVHGLPAGGAVKTE 1004
 RESULT 13
 NP14-RAT STANDARD: PRT: 704 AA.
 AC P41777:
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE 140 KDA NUCLEOLAR PHOSPHOPROTEIN (NOP140).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601.
 RC TISSUE-LIVER;
 RA MEDLINE: 92333542.
 RA Meier U.T., Blobel G.;
 RT Cell 70:127-138(1992)
 RL "NOP140 shuttles on tracks between nucleolus and cytoplasm."
 CC
 CC -1- FUNCTION: MAY FUNCTION AS A CHAPERONE FOR IMPORT INTO AND/OR FROM
 CC THE NUCLEOLUS. IT COULD FUNCTION TO COVER AND NEUTRALIZE HIGHLY
 CC CHARGED DOMAINS OF PERIBIOSOMAL PARTICLES (EXPORT) OR OF RIBOSOMAL
 CC PROTEINS (IMPORT). BINDS NUCLEAR LOCALIZATION SEQUENCES; THE
 CC BINDING TO SUCH SEQUENCES IS DEPENDENT ON PHOSPHORYLATION. THE
 CC STATE OF PHOSPHORYLATION MAY REPRESENT A MEANS OF REGULATING THE
 CC PROTEIN'S AFFINITY FOR NLS-CONTAINING PROTEINS AND THEREBY ITS
 CC ABILITY TO FUNCTION IN NUCLEOCYTOPLASMIC TRANSPORT.
 CC -1- SUBCELLULAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN
 CC NUCLEOLUS AND CYTOPLASM. THESE TRACKS EXTEND FROM THE DENSE
 CC FIBRILLAR COMPONENT OF THE NUCLEOLUS ACROSS THE NUCLEOLAR PLASM TO
 CC A LIMITED NUMBER OF NUCLEAR PORE COMPLEXES.
 CC -1- PIM: THIS PROTEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND
 CC DEPHOSPHORYLATION ON CR-II AND PGC SITES. NOP140 IS ONE OF THE
 CC MOST PHOSPHORYLATED PROTEINS IN THE CELL.
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 CC -----
 DR EMBL: M94287; AAA41718.1; -;
 DR EMBL: M94288; AAA41719.1; -;
 KW Nuclear Protein; Phosphorylation; Repeat; Chaperone; Transport.
 FT DOMAIN 84 570
 FT
 FT REPEAT 84 95
 FT REPEAT 127 138
 FT REPEAT 170 181
 FT REPEAT 231 242
 FT REPEAT 274 285
 FT REPEAT 335 346
 FT REPEAT 373 384
 FT REPEAT 434 445
 FT REPEAT 479 490
 FT REPEAT 524 535
 FT REPEAT 559 570
 FT VARIANT 150 150
 FT MOD.RES 567 567
 FT DOMAIN 126 131
 FT DOMAIN 136 140
 FT DOMAIN 141 146
 FT DOMAIN 226 236
 FT DOMAIN 274 277
 FT DOMAIN 283 287
 FT DOMAIN 432 435
 FT DOMAIN 439 442
 POLY-SER.
 POLY-GLU.
 POLY-LYS.
 POLY-SER.
 POLY-SER.
 POLY-GLU.
 POLY-SER.
 POLY-SER.
 POLY-SER.

FT DOMAIN 478 487
 FT DOMAIN 521 528
 FT DOMAIN 566 572
 SO SEQUENCE 704 AA; 73562 MW; 14DF1BF2DE483EA3 CRC64;
 Query Match 7.6%; Score 175.5; DB 1; Length 704;
 Best Local Similarity 21.7%; Pred. No. 0.049;
 Matches 99; Conservative 60; Mismatches 183; Indels 115; Gaps 18;
 OY 44 KESLQRTEDSGSEPESESTDAKSTPTADYAPLVDBEAPKQAAQPH-----TEIP 98
 DB 76 KKAKERTSSSSSD--SSEEDKAQVPTQ-----AAPAKRASLPQAGRAAAKAS 126
 OY 99 EGTAEEAGIDPTSLDEAAGHYTQARVSKSKDGTSGDSKRAKAGDKTKIATPGAA 158
 DB 127 ESSSESESEEE---EKDKKKRVQOKAVKPAKAVRPPKRAESESSED--SSSEDA 182
 OY 159 PPGKGQANATRIPAKT-----PPAPTPPSGEPSPGSGRSGISPGSPGTGSRNRT 213
 DB 183 POTOAKPAATAAPAKPTKATKAPKPPAKAPKAAKAGKAGSSSSSSSSSDSEEE 242
 OY 214 SLPTPTRE--PKRVAVRTPPK-----SPSASKSLQTA-----V 248
 DB 243 KKAAPLKTAPKQVAVKAVKTAAPTKOSSSESDSSSEEBQKKPKKRAAGPYSSV 302
 OY 249 PMPDLKWKSKTG-----STENLKHPG-----GKV 275
 DB 303 PPSVSLSKKVGQNSPKKAAQTPADSSADSESDSSSEEEKRPATVYKTPAKP 362
 OY 276 QIINKKIDLSNVOSKSGKDNKIHVPGGGSVOIYKPVLSK-----VTSKCSLGN 328
 DB 363 APVKKKAESDSSSDSSSED-----EAPAKVSAKTSPLSKPATVPPPAKAV 412
 OY 329 --HHKPGGQVEYSEKIDFKRVOSKISLNDITHVPGGKNKIEHKITFENAKAT 386
 DB 413 ATPQAPGSGKPPSKRADSSSESESESEENT-----KKSVTTPKA--RYTAKAP 464
 OY 387 DHGAEIYKSPVVSADTSPRHLNVSVSTGSDVWYDSP 423
 DB 465 SLPAK---QAPRAGDSS---SDSESSSEEEKTP 494
 RESULT 14
 NFM-CHICK STANDARD: PRT: 857 AA.
 AC P16053:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE NEUROFILAMENT TRIPLET M PROTEIN (160 KDA NEUROFILAMENT PROTEIN)
 DE (NF-M).
 OS NFM.
 OC Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 90174973.
 RA Zopf D., Dineva B., Betz H., Gundelfinger E.D.;
 RT "Isolation of the chicken middle-molecular weight neurofilament
 RT (NF-M) gene and characterization of its promoter."
 RT Nucleic Acids Res. 18:521-529(1990).
 RL [2]
 RP SEQUENCE OF 259-857 FROM N.A.
 RA MEDLINE: 88112814.
 RA Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.;
 RT "Identification of gene products expressed in the developing chick
 RT visual system: characterization of a middle-molecular-weight
 RT neurofilament cDNA."
 RL Genes Dev. 1:699-708(1987).
 CC
 CC -1- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,


```

QY 94 HTEIPEGTTAEAG-----IGDTPS-----LEDEAA----- 119
Db 154 KTWIPLRNTCPCLNTPVAYLLVGTASGFSFTIPVNDPRTRVLEAAVRAAGTAVDFIWT 213
QY 120 -----GHVTOARVSKSKDGTGSDDKAKAGADGKTIATPRGAAPPQKGA 166
Db 214 GNPRTA PRSLGCHTVRA--LSPTPPWPGTDEDDDLADVDVYPAPR-RAPRRGGGA 270
QY 167 NATR---IPAKTPPAKTPP-----SSGEPKSGDRSGYSSPSPGTGSRSRTPSLP--- 216
Db 271 GATRGTSOPAPATRPAPPEAGPRSSSSGGAPLRAGVSG--SGGGPAAVAVPRAVSLPPAA 328
QY 217 -----TPPTREPK-----KVAVVTRTPPKSPSSAKSRLQTAPVPM 251
Db 329 GCGRAQARRVGEDAAAAGRTTPPARAQPRAAQEPPIVISDSPPPSP-----RRPAGPGPLS 383
QY 252 DLKVVKSKIGSTENLKHOPGGG 273
Db 384 FVSSSSAOVSS-----GPGGG 399

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Search completed: September 28, 2000, 20:03:59
 Job time: 287 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2000, 19:58:24 ; Search time 49.63 Seconds
(without alignments)
616.086 Million cell updates/sec

Title: US-09-142-613-1

Perfect score: 1 MAEPKREFVEMEDHAGQDTY.....SPQATLADVSASIAKQGL 441

Sequence: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scoring table: 225878 segs, 69334122 residues

Searched: Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPREMBL.12:*
1: sp.Archea:*
2: sp.Bacteria:*
3: sp.Fungi:*
4: sp.Human:*
5: sp.Invertebrate:*
6: sp.Mammal:*
7: sp.Mhc:*
8: sp.Organelle:*
9: sp.Phage:*
10: sp.Plant:*
11: sp.Potent:*
12: sp.Virus:*
13: sp.Vertebrate:*
14: sp.Unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1993.5	86.9	430	11 060684	060684 mus musculus
2	1878	81.8	402	6 002828	002828 capra hircu
3	1861.5	81.1	686	11 063567	063567 rattus norv
4	1710.5	74.5	374	11 063677	063677 rattus norv
5	1698.5	74.0	372	11 060685	060685 mus musculus
6	1659.5	72.3	416	6 028187	028187 mus taurus
7	1587.5	69.2	350	11 060686	060686 mus musculus
8	1524	66.4	369	6 028185	028185 bos taurus
9	1415	61.7	347	6 028188	028188 bos taurus
10	1410	61.4	365	6 028186	028186 bos taurus
11	1337.5	58.3	338	6 028190	028190 bos taurus
12	1328.5	53.5	316	6 028189	028189 bos taurus
13	717.5	31.3	1835	11 064715	064715 rattus norv
14	714	31.1	1828	11 063724	063724 rattus norv
15	710	30.9	333	6 028869	028869 bos taurus
16	690.5	30.1	198	11 067749	067749 rattus norv
17	626	27.3	124	11 062286	062286 mus musculus
18	546	23.8	381	11 064710	064710 rattus norv
19	545	23.7	1152	4 013082	013082 homo sapien

20	481	21.0	125	4	016296	016296 homo sapien
21	403.5	17.6	1224	13	091190	091190 xenopus lae
22	364.5	15.9	431	5	017364	017364 caenorhabd
23	364.5	15.9	453	5	002592	002592 caenorhabd
24	347	15.1	113	13	012967	012967 fugu rubrip
25	329.5	14.4	413	5	P90973	P90973 caenorhabd
26	328	14.3	436	5	017365	017365 caenorhabd
27	278	12.1	242	5	020350	020350 caenorhabd
28	246.5	10.7	928	13	098906	098906 gallus gal
29	193.5	8.4	1560	11	088323	088323 mus musculu
30	192	8.4	2187	11	P70670	P70670 mus musculu
31	184.5	8.0	1211	11	035233	035233 mus musculu
32	183.5	8.0	813	2	050279	050279 mycoplasma
33	181.5	7.9	1566	4	043810	043810 homo sapien
34	181.5	7.9	1581	4	075447	075447 homo sapien
35	179	7.8	3507	5	023587	023587 caenorhabd
36	178	7.8	971	5	09XV54	09XV54 caenorhabd
37	177.5	7.7	487	13	073793	073793 serinus can
38	176	7.7	990	13	091803	091803 xenopus lae
39	173.5	7.6	2441	5	096124	096124 plasmidium
40	173	7.5	810	6	077788	077788 bos taurus
41	173	7.5	903	5	017917	017917 caenorhabd
42	172.5	7.5	455	5	004961	004961 plasmidium
43	172.5	7.5	880	5	017338	017338 caenorhabd
44	172.5	7.5	930	5	017339	017339 caenorhabd
45	172	7.5	744	2	069995	069995 streptomyce

ALIGNMENTS

RESULT 1
ID 060684 PRELIMINARY; PRT; 430 AA.
AC 060684;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE MICROBUBULE-ASSOCIATED PROTEIN TAU ISOFORM 23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HIM OF1 SP; TISSUE=LIVER;
RA KENNER L., EFERL R., ZATLOUKAL K., HOEFER G., DENK H.;
RL Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12914; AAA58343.1;
DR PROSITE: P500229; TRO_MAP; 4;
DR PFM; PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 430 AA; 44893 MW; FDS2F55A CRC32;

Query Match	86.9%	Score 1993.5;	DB 11;	Length 430;
Best Local Similarity	87.9%	Pred. No. 6.5e-119;		
Matches 391;	Conservative 16;	Mismatches 19;	Indels 19;	Gaps 4;
QY 1	MAEPKREFVEMEDHAGQDTYGLGRKDGTYM--HOEGDTAGLKESPLQPTEDGSPE 58			
DB 1	MADPREFVEMEDHAD-----YTLDDQEDMDHGLKESPPPADGAE 47			
QY 59	PGSETDAKSTPAEDYTAFLVDGAPGKQAAOPTEIPEGTTAEAGIGPSTLEDA 118			
DB 48	PGSETDAKSTPAEDYTAFLVDGAPGKQAAOPTEIPEGTTAEAGIGPSTLEDA 107			
QY 119	AGHTVQARVYSKSGDGDKKAKAGDGT--KATPRGAAPPGQGAANTRIPAKTP 176			
DB 108	AGHTVQARVYS--SKDRTGDEKKAKAGDGTGAKIATPRGAAPGQGSNATRIIPAKTP 165			
QY 177	PAKTPPSGSGPPKSGDRGSGSPGSPGSRSPSPSPPTPEPRKVVAVRRPPKSP 236			
DB 166	PSKTPPSGSGPPKSGDRGSGSPGSPGSRSPSPSPPTPEPRKVVAVRRPPKSP 225			


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QY 237 SSASRLQTAAPVPMPLDKNVKSKIGSTENLKHOPGGGVQIINKLDSLNVQSGSKSDN 296
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 226 SASRRLQTAAPVPMPLDKNVKSKIGSTENLKHOPGGGVQIINKLDSLNVQSGSKSDN 285
QY 297 IKHPGGGSVOIVYKPPDLSKVTSKCSGLGNIHKHPGGGVQEVSEKLDFFDRVQSKIGS 356
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 286 IKHPGGGSVOIVYKPPDLSKVTSKCSGLGNIHKHPGGGVQEVSEKLDFFDRVQSKIGS 345
QY 357 LDNTHTVPGGNGKKTETHTKLFRENAKAKTDHGAELIYKSPVSGDTPRHLSNVSGTGS 416
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 346 LDNTHTVPGGNGKKTETHTKLFRENAKAKTDHGAELIYKSPVSGDTPRHLSNVSGTGS 405
QY 417 IDWVDSPOLATLADVSASLAKOGL 441
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 406 IDWVDSPOLATLADVSASLAKOGL 430

RESULT 2
002828 PRELIMINARY; PRT; 402 AA.
ID 002828:
AC 002828:
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
OS Capra hircus (goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Capra.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN CORTEX;
RX MEDLINE; 97012131.
RA NELSON P.T., STEFANSSON K., GULCHER J., SAPER C.B.;
RT "Molecular evolution of tau protein: implications for Alzheimer's
RL disease."
RL J. Neurochem. 67:1622-1632(1996).
CC -1- FUNCTION: HEAT STABLE PROTEIN WHICH PROMOTES MICROTUBULE ASSEMBLY
CC AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND
CC MAINTENANCE OF NEURONAL POLARITY. BINDS AND STABILIZES AXONAL
CC MICROTUBULES WHICH IS IMPORTANT FOR MAINTAINING AXONAL TRANSPORT
CC AND DEFINING THE POLARITY OF A NEURON. AXONAL POLARITY IS
CC DETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
CC DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME.
CC -1- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST TWO DIFFERENT ISOFORMS: TAU-A AND
CC TAU-B (SHOWN HERE); OF TAU ARE PRODUCED BY DEVELOPMENTALLY AND
CC TISSUE-SPECIFICALLY CONTROLLED ALTERNATIVE SPLICING. THEY DIFFER
CC FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS/INSERTS,
CC ONE CONTAINING THE ADDITIONAL TAU/MAP REPEAT. SHORT FORMS ALLOW
CC PLASTICITY OF THE CYTOSKELETON WHEREAS LONGER FORMS MAY
CC REPRESENTATIVELY PLAY A ROLE IN ITS STABILIZATION.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN. TYPE I TAU CONTAINS
CC THREE REPEATS WHILE TYPE II TAU CONTAINS FOUR REPEATS.
CC -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
CC S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (CDK2, GSK3)
CC (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN MITOSIS), AND AT
CC SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-
CC REGULATING KINASE (MARK).
CC -1- SIMILARITY: CONTAINS 4 OR 5 TAU/MAP REPEATS, FROM WHICH ONE IS
CC APPROXIMATE, DEPENDENT ON THE ISOFORM.
DR EMBL; S83347; AAB50785.1; -.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFM; PFM00418; tubulin-binding; 4.
KM Microtubules; Repeat; Alternative splicing; Cytoskeleton; Acetylation;
KM phosphorylation.
FT INIT_MET 0
FT MOD_RES 1
FT REPEAT 213
FT REPEAT 243
FT REPEAT 244
FT REPEAT 274
FT REPEAT 275
FT REPEAT 305
FT REPEAT 306
FT REPEAT 337
      TAU/MAP MOTIF.
      TAU/MAP MOTIF.
      TAU/MAP MOTIF.

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FT DISUFIID 252 283
FT MOD_RES 223 223
FT MOD_RES 254 254
FT MOD_RES 285 285
FT MOD_RES 317 317
FT VARSPLOC 33 61
FT VARSPLOC 266 266
SQ SEQUENCE 402 AA; 41716 MW; FCLE79AB CRC32;

Query Match 81.8%; Score 1878; DB 6; Length 402;
Best Local Similarity 84.4%; Pred No. 1,2e-111;
Matches 374; Conservative 8; Mismatches 17; Indels 44; Gaps 4;

QY 2 AEPQEFVNEHDAAGDTYGLGDRKDGGTYMH-QGDDTDAGIKESPLQTPREDGSEERG 60
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 1 AEPQEFVNEHDAAGDTYGLGDRKDGGTYMH-QGDDTDAGIKESPLQTPREDGSEERG 48
QY 61 SETSDAKSTPTADVTATPLVDGAPGKQAAAPHTETPEGTAAEAGIGDTPSLDEAAG 120
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 49 SETSDAKSTPTAE-----AEEAGIGDTPSLDEAAG 79
QY 121 HVTQARVYKSKDGTGSDOKKAKGADGK--TKIATPRGAAPGQKQANATRIAPKTPA 178
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 80 HVTQARVYKSKDGTGSDOKKAKGADGKPEKTIATPRGAAPGQKQANATRIAPKTPA 139
QY 179 PKTPSSGEPKSGDRSGYSSPGSPGTSRSKTPSLPTPTREPKVAVVTTPKSPSS 238
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 140 PKTSPGSGEGSGKSGDSSGSSPSGTPGSRSTPLPTPTREPKVAVVTTPKSPSA 199
QY 239 AKSRLQTAAPVPMPLDKNVKSKIGSTENLKHOPGGGVQIINKLDSLNVQSGSKSDN 298
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 200 AKSRLQTAAPVPMPLDKNVKSKIGSTENLKHOPGGGVQIINKLDSLNVQSGSKSDN 259
QY 299 HVPGGGSVOIVYKPPDLSKVTSKCSGLGNIHKHPGGGVQEVSEKLDFFDRVQSKIGSD 358
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 260 HVPGGGSVOIVYKPPDLSKVTSKCSGLGNIHKHPGGGVQEVSEKLDFFDRVQSKIGSD 319
QY 359 NITHVPGGNGKKTETHTKLFRENAKAKTDHGAELIYKSPVSGDTPRHLSNVSGTGSID 418
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 320 NITHVPGGNGKKTETHTKLFRENAKAKTDHGAELIYKSPVSGDTPRHLSNVSGTGSID 379
QY 419 MDVSPQATLADVSASLAKOGL 441
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 380 MDVSPQATLADVSASLAKOGL 402

RESULT 3
063567 PRELIMINARY; PRT; 686 AA.
ID 063567:
AC 063567:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE BIG TAU.
GN TAU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 92179305.
RA GOEDERT M., SPILLANTINI M.G., CROWTHER R.A.;
RT "Cloning of a big tau microtubule-associated protein characteristic of
RT the peripheral nervous system."
RT Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
DR EMBL; M84156; AAA42204.1; -.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFM; PFM00418; tubulin-binding; 4.
KM Microtubules; Repeat.
SQ SEQUENCE 686 AA; 71774 MW; 70992021 CRC32;

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DB 1 MADPROEFTMEDHAGD-----YTLDDQEGMDHGLK----- 33
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPEGTAEEAGIGDTPSLEDEA 118
 DB 34 -----AEEAGIGDTPNOEDQA 49
 QY 119 AGHTVQARVMYSKSDGTGSDDKAKAGADGKT--KIATPRGAAPPGQKQANATRIIPAKTP 176
 DB 50 AGHTVQARVA--SKDRTGNDKKAKAGADGKTGAKIATPRGAASPAOKGTSNATRIIPAKTT 107
 QY 177 PAPKTPPSSGEPKSGDRSGYSSPGSPGTSRSTRPLPTPTREPKVAAYVTRPPSP 236
 DB 108 PPKTPPSSGEPKSGDRSGYSSPGSPGTSRSTRPLPTPTREPKVAAYVTRPPSP 167
 QY 237 SSKSRRLQTAAPYMPDLKKNVSKISTENLKHQPGGKQIINKKLDLSNVOSKSGSKDN 296
 DB 168 SSKSRRLQTAAPYMPDLKKNVSKISTENLKHQPGGKQIINKKLDLSNVOSKSGSKDN 227
 QY 297 IKHVPGGSVQIVYKPVDSLKYTSKSGSLGNTHHKPGGQVEVSEKLDKRVOSKIGS 356
 DB 228 IKHVPGGSVQIVYKPVDSLKYTSKSGSLGNTHHKPGGQVEVSEKLDKRVOSKIGS 287
 QY 357 LDNTHVPGGSKKLTETHKLTFRENAKAKTDHGAETVYKSPVSGDTSRHLTSNVSGS 416
 DB 288 LDNTHVPGGSKKLTETHKLTFRENAKAKTDHGAETVYKSPVSGDTSRHLTSNVSGS 347
 QY 417 IDNVSPQATLADDEVASASIAKQGL 441
 DB 348 IDNVSPQATLADDEVASASIAKQGL 372

RESULT 6
 Q28187
 ID 028187 PRELIMINARY: PRT: 416 AA.
 AC 028187:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TAU PROTEIN.
 GN TAU.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovine; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261765.
 RA HIMMLER A.; DRECHSEL D.; KIRSCHNER M.W.; MARTIN D.W.;
 RT "Tau consists of a set of proteins with repeated C-terminal
 RT microtubule-binding domains and variable N-terminal domains.";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261766.
 RA HIMMLER A.;
 RT "Structure of the bovine tau gene: alternatively spliced transcripts
 RT generate a protein family.";
 RL Mol. Cell. Biol. 9:1389-1396(1989).
 RN [3]
 DR EMBL: M26178; AAAS1601.1; JOINED.
 DR EMBL: L34840; AAAS1601.1; JOINED.
 DR EMBL: L34841; AAAS1601.1; JOINED.
 DR EMBL: L34842; AAAS1601.1; JOINED.
 DR EMBL: L34843; AAAS1601.1; JOINED.
 DR EMBL: L34844; AAAS1601.1; JOINED.
 DR EMBL: L34845; AAAS1601.1; JOINED.
 DR EMBL: L34846; AAAS1601.1; JOINED.
 DR EMBL: L34847; AAAS1601.1; JOINED.
 DR EMBL: L34848; AAAS1601.1; JOINED.
 DR EMBL: L34849; AAAS1601.1; JOINED.
 DR EMBL: L34950; AAAS1601.1; JOINED.
 DR EMBL: L34951; AAAS1601.1; JOINED.
 DR PROSITE: PS00229; TAU MAP: 4.
 DR PFM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat.

SO SEQUENCE 416 AA; 42848 MW; A57504F7 CRC32;
 Query Match 72.3%; Score 1659.5; DB 6; Length 416;
 Best Local Similarity 84.3%; Pred. No. 7.9e-98;
 Matches 328; Conservative 9; Mismatches 21; Indels 31; Gaps 4;
 QY 1 MAEPROEFTMEDHAGD-----YTLDDQEGMDHGLK----- 33
 DB 1 MAEPROEFTMEDHAGD-----YTLDDQEGMDHGLK----- 33
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPEGTAEEAGIGDTPSLEDEA 118
 DB 34 -----YTLDDQEGMDHGLK----- 33
 QY 119 AGHTVQARVMYSKSDGTGSDDKAKAGADGKT--KIATPRGAAPPGQKQANATRIIPAKTP 176
 DB 50 AGHTVQARVA--SKDRTGNDKKAKAGADGKTGAKIATPRGAASPAOKGTSNATRIIPAKTT 107
 QY 177 PAPKTPPSSGEPKSGDRSGYSSPGSPGTSRSTRPLPTPTREPKVAAYVTRPPSP 236
 DB 108 PPKTPPSSGEPKSGDRSGYSSPGSPGTSRSTRPLPTPTREPKVAAYVTRPPSP 167
 QY 237 SSKSRRLQTAAPYMPDLKKNVSKISTENLKHQPGGKQIINKKLDLSNVOSKSGSKDN 296
 DB 168 SSKSRRLQTAAPYMPDLKKNVSKISTENLKHQPGGKQIINKKLDLSNVOSKSGSKDN 227
 QY 297 IKHVPGGSVQIVYKPVDSLKYTSKSGSLGNTHHKPGGQVEVSEKLDKRVOSKIGS 356
 DB 228 IKHVPGGSVQIVYKPVDSLKYTSKSGSLGNTHHKPGGQVEVSEKLDKRVOSKIGS 287
 QY 357 LDNTHVPGGSKKLTETHKLTFRENAKAKTDHGAETVYKSPVSGDTSRHLTSNVSGS 416
 DB 288 LDNTHVPGGSKKLTETHKLTFRENAKAKTDHGAETVYKSPVSGDTSRHLTSNVSGS 347
 QY 417 IDNVSPQATLADDEVASASIAKQGL 441
 DB 348 IDNVSPQATLADDEVASASIAKQGL 372

RESULT 7
 Q60686
 ID 060686 PRELIMINARY: PRT: 350 AA.
 AC 060686:
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HIN OF1 SPF, TISSUE=LIVER;
 RA KENNER L.; EBERL R.; ZATLOUKAL K.; HOEFLER G.; DENK H.;
 RL Submitted (MGC-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12916; AAAS345.1; JOINED.
 DR PROSITE: PS00229; TAU MAP: 4.
 DR PFM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat.
 SO SEQUENCE 350 AA; 36740 MW; 9C54BC5E CRC32;
 Query Match 69.2%; Score 1587.5; DB 11; Length 350;
 Best Local Similarity 72.4%; Pred. No. 2.3e-93;
 Matches 322; Conservative 12; Mismatches 12; Indels 99; Gaps 5;
 QY 1 MAEPROEFTMEDHAGD-----YTLDDQEGMDHGLK----- 33
 DB 1 MAEPROEFTMEDHAGD-----YTLDDQEGMDHGLK----- 33
 QY 59 PGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAOPHTIEPEGTAEEAGIGDTPSLEDEA 118
 DB 34 -----YTLDDQEGMDHGLK----- 33
 QY 119 AGHTVQARVMYSKSDGTGSDDKAKAGADGKT--KIATPRGAAPPGQKQANATRIIPAKTP 176
 DB 50 AGHTVQARVA--SKDRTGNDKKAKAGADGKTGAKIATPRGAASPAOKGTSNATRIIPAKTT 107

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Db 34 -----AAVA--SKD--NDKAKAGADGKATATPRGAASPAOKTSMATRIPAKTT 85
QY 177 PAPKTPSSGSGPPKSGDGRSGYSSPGSPGTGSGSRSGSPSLPTPTREPKAVVVRTPPKSP 236
    |||||
Db 86 PSPKTPPSGSGPPKSGDGRSGYSSPGSPGTGSGSRSGSPSLPTPTREPKAVVVRTPPKSP 145
    |||||
QY 237 SSASRLQTAIVPMPDLKNVSKSIGSTENLKHOPGGGVQVQIINKLDSLNVOSKSGSKDN 296
    |||||
Db 146 SASKRLQTAIVPMPDLKNVSKSIGSTENLKHOPGGGVQVQIINKLDSLNVOSKSGSKDN 205
    |||||
QY 297 IKHPVGGGSGVQIVKPPVDSLKVTSGKSLGNIHHRKPGGGGVQVQVSEKIDFDRVQSKIGS 356
    |||||
Db 206 IKHPVGGGSGVQIVKPPVDSLKVTSGKSLGNIHHRKPGGGGVQVQVSEKIDFDRVQSKIGS 265
    |||||
QY 357 LDNTHVPGGNGKRIETKLTFRENAKAKTDHGAETIVKSPVSGDTPSRHLSNVSTGS 416
    |||||
Db 266 LDNTHVPGGNGKRIETKLTFRENAKAKTDHGAETIVKSPVSGDTPSRHLSNVSTGS 325
    |||||
QY 417 IDWVDSPLQATLADDEVASLAKOGL 441
    |||||
Db 326 IDWVDSPLQATLADDEVASLAKOGL 350
    |||||

RESULT 8
Q28185 PRELIMINARY; PRT; 369 AA.
ID Q28185;
AC Q28185;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA HIMMER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261766.
RA HIMMER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
RT generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; L34940; AAA51602.1; JOINED.
DR EMBL; L34941; AAA51602.1; JOINED.
DR EMBL; L34943; AAA51602.1; JOINED.
DR EMBL; L34944; AAA51602.1; JOINED.
DR EMBL; L34946; AAA51602.1; JOINED.
DR EMBL; L34948; AAA51602.1; JOINED.
DR EMBL; L34949; AAA51602.1; JOINED.
DR EMBL; L34950; AAA51602.1; JOINED.
DR EMBL; L34951; AAA51602.1; JOINED.
DR EMBL; L34951; AAA51602.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFAM; PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 369 AA; 38212 MW; 948F16BD CRC32;

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Query Match 66.4%; Score 1524; DB 6; Length 369;
Best Local Similarity 81.8%; Pred. No. 2.5e-89;
Matches 305; Conservative 6; Mismatches 16; Indels 46; Gaps 5;
QY 1 MAEPROFEFVEMEDHAGODTYGLGRKDOGGYTMH-QEGDITDAKRESPLQTPTEDSSEEP 59
    |||||
Db 1 MAEPROFEFVEMEDHAGODTYGLGRKDOGGYTMH-QEGDITDAKRESPLQTPTEDSSEEP 48
    |||||

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QY 60 GSETSDAKSPTPTADVYTAPLYDEGAPGKQAAOAPHTPIPEGTTAEAGISDTPSELEDEAA 119
    |||||
Db 49 GSETSDAKSPTPTADVYTAPLYDEGAPGKQAAOAPHTPIPEGTTAEAGISDTPSELEDEAA 79
    |||||
QY 120 GHVTAQAVVSKSKDGTSDSKAKAGADGK--TKATATPRGAAPPQOKQOANATRIAPAKTP 177
    |||||
Db 80 GHVTAQAVVSKSKDGTSDSKAKAGADGK--TKATATPRGAAPPQOKQOANATRIAPAKTP 139
    |||||
QY 178 AKPTPPSSGSGPPKSGDGRSGYSSPGSPGTGSGSRSGSPSLPTPTREPKAVVVRTPPKSP 237
    |||||
Db 140 TPKTSP--GSGKSGDGRSGYSSPGSPGTGSGSRSGSPSLPTPTREPKAVVVRTPPKSP 197
    |||||
QY 238 SASKRLQTAIVPMPDLKNVSKSIGSTENLKHOPGGGVQVQIINKLDSLNVOSKSGSKDN 297
    |||||
Db 198 AAKSRLQTAIVPMPDLKNVSKSIGSTENLKHOPGGGVQVQIINKLDSLNVOSKSGSKDN 257
    |||||
QY 298 KHPVGGGSGVQIVKPPVDSLKVTSGKSLGNIHHRKPGGGGVQVQVSEKIDFDRVQSKIGSL 357
    |||||
Db 258 KHPVGGGSGVQIVKPPVDSLKVTSGKSLGNIHHRKPGGGGVQVQVSEKIDFDRVQSKIGSL 317
    |||||
QY 358 DNTHVPGGNGK 370
    |||||
Db 318 DNTHVPGGNGK 330
    |||||

RESULT 9
Q28188 PRELIMINARY; PRT; 347 AA.
ID Q28188;
AC Q28188;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA HIMMER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261766.
RA HIMMER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
RT generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; L34940; AAA51605.1; JOINED.
DR EMBL; L34941; AAA51605.1; JOINED.
DR EMBL; L34943; AAA51605.1; JOINED.
DR EMBL; L34944; AAA51605.1; JOINED.
DR EMBL; L34946; AAA51605.1; JOINED.
DR EMBL; L34948; AAA51605.1; JOINED.
DR EMBL; L34949; AAA51605.1; JOINED.
DR EMBL; L34950; AAA51605.1; JOINED.
DR EMBL; L34951; AAA51605.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFAM; PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 347 AA; 36016 MW; 00FD6406 CRC32;

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Query Match 61.7%; Score 1415; DB 6; Length 347;
Best Local Similarity 76.7%; Pred. No. 1.8e-82;
Matches 286; Conservative 4; Mismatches 15; Indels 68; Gaps 5;
QY 1 MAEPROFEFVEMEDHAGODTYGLGRKDOGGYTMH-QEGDITDAKRESPLQTPTEDSSEEP 59
    |||||

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Db 1 MAEPROEFVMEDEHA-----OGDYTLDOQEGMDGLKESPLQTPADGSEEP 48
QY 60 GSETSDAKSTPTAEDVTAPLVDEGAPKQAAQPHTEIPEGTAEBAGIGDTPSLEDEAA 119
Db 49 GSETSDAKSTPTA----- 62
QY 120 GHVTAARVYVSKSDGTSGDDKKAKGADG--TKIATPRGAAPPGQKQANATRIAPAKTP 177
Db 63 -----ARVYVSKGDKGTGDDKKTKGADGKPTKIATPRGAAPPGQKQANATRIAPAKTP 117
QY 178 APTKPPSGEPKSGDRSGYSSPGSPGTPGSRSTPSLPTPTREPKVAVVTRTPKSPS 237
Db 118 TPKTSP--GESGSGDRSGYSSPGSPGTPGSRSTPSLPTPTREPKVAVVTRTPKSPS 175
QY 238 SAKSRLQAPVMPDLKLVKSKIGSTENLKHQPGGKVOIINKLIDLSNVOSKSGSKDI 297
Db 176 AAKSRLQAPGMPDLKLVKSKIGSTENLKHQPGGKVOIINKLIDLSNVOSKSGSKDI 235
QY 298 KHPVGGGVQIYKRPVDSLKTSKCGSLGNHHRKPGGGGVVEYKSEKLDKRVQSKIGSL 357
Db 226 KHPVGGGVQIYKRPVDSLKTSKCGSLGNHHRKPGGGGVVEYKSEKLDKRVQSKIGSL 295
QY 358 DNITHVPGGKNK 370
Db 296 DNITHVPGGKNK 308

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RESULT 10

Q28186 ID Q28186 PRELIMINARY; PRT; 365 AA.

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AC Q28186;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA HINMELER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "Tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA HINMELER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; M26178; AAAS1604.1; -
DR EMBL; L34940; AAAS1604.1; JOINED.
DR EMBL; L34941; AAAS1604.1; JOINED.
DR EMBL; L34944; AAAS1604.1; JOINED.
DR EMBL; L34946; AAAS1604.1; JOINED.
DR EMBL; L34947; AAAS1604.1; JOINED.
DR EMBL; L34948; AAAS1604.1; JOINED.
DR EMBL; L34949; AAAS1604.1; JOINED.
DR EMBL; L34950; AAAS1604.1; JOINED.
DR EMBL; L34951; AAAS1604.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFAM; PF00418; tubulin-binding; 4.
DR Microtubules; 3.
KW Microtubules.
SQ SEQUENCE 365 AA; 37923 MW; 08A4187E CRC32;

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Query Match 61.4%; Score 1410; DB 6; Length 365;
Best Local Similarity 73.5%; Pred. No. 4e-82;

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Matches 286; Conservative 6; Mismatches 15; Indels 82; Gaps 5;
QY 1 MAEPROEFVMEDEHAGDITGLGDRKDGGYTMH--QEGDTDAGLKESPLQTPEDGSEEP 59
Db 1 MAEPROEFVMEDEHA-----OGDYTLDOQEGMDGLKESPLQTPADGSEEP 48
QY 60 GSETSDAKSTPTAEDVTAPLVDEGAPKQAAQPHTEIPEGTAEBAGIGDTPSLEDEAA 119
Db 49 GSETSDAKSTPTA----- 62
QY 120 GHVTAARVYVSKSDGTSGDDKKAKGADG--TKIATPRGAAPPGQKQANATRIAPAKTP 177
Db 63 -----ARVYVSKGDKGTGDDKKTKGADGKPTKIATPRGAAPPGQKQANATRIAPAKTP 117
QY 178 APTKPPSGEPKSGDRSGYSSPGSPGTPGSRSTPSLPTPTREPKVAVVTRTPKSPS 221
Db 118 TPKTSPATMOYQKPPRPAAGAKSERGESGSDRSGYSSPGSPGTPGSRSTPSLPTPTR 177
QY 222 EPRKVAVVRTPPKSPSSAKSRLQAPVMPDLKLVKSKIGSTENLKHQPGGKVOIINK 281
Db 178 EPRKVAVVRTPPKSPSAKSLQAPGMPDLKLVKSKIGSTENLKHQPGGKVOIINK 237
QY 282 LDLSNVOSKSGSKDNIHVPVGGGVQIYKRPVDSLKTSKCGSLGNHHRKPGGGGVVEYKS 341
Db 238 LDLSNVOSKSGSKDNIHVPVGGGVQIYKRPVDSLKTSKCGSLGNHHRKPGGGGVVEYKS 297
QY 342 EKLDFKRVOSKIGSLDNITHVPGGKNK 370
Db 298 EKLDFKRVOSKIGSLDNITHVPGGKNK 326

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RESULT 11

Q28190 ID Q28190 PRELIMINARY; PRT; 338 AA.

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AC Q28190;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA HINMELER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "Tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA HINMELER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; M26178; AAAS1603.1; -
DR EMBL; L34940; AAAS1603.1; JOINED.
DR EMBL; L34941; AAAS1603.1; JOINED.
DR EMBL; L34944; AAAS1603.1; JOINED.
DR EMBL; L34946; AAAS1603.1; JOINED.
DR EMBL; L34948; AAAS1603.1; JOINED.
DR EMBL; L34950; AAAS1603.1; JOINED.
DR EMBL; L34951; AAAS1603.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 3.
DR PFAM; PF00418; tubulin-binding; 3.
DR Microtubules; Repeat.
KW Microtubules.
SQ SEQUENCE 338 AA; 34965 MW; F349F977 CRC32;

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Query Match 58.3%; Score 1337.5; DB 6; Length 338;
 Best Local Similarity 73.5%; Pred. No. 1,4e-77;
 Matches 214; Conservative 6; Mismatches 16; Indels 77; Gaps 6;

QY 1 MAEPREFEWMEDHAGODTYGLDRKDGQGYTMH-OEGDTDAGLKESPLQTPTEDESGEEP 59
 DB 1 MAEPREFEWMEDHAGODTYGLDRKDGQGYTMH-OEGDTDAGLKESPLQTPTEDESGEEP 48
 QY 60 GSETSDAKSTPTAEADYTAFLVDEGAPGKQAAAPHTETPEGTAEAGIGDTPSLEDEA 119
 DB 49 GSETSDAKSTPTAEADYTAFLVDEGAPGKQAAAPHTETPEGTAEAGIGDTPSLEDEA 79
 QY 120 GHYTOARMVSKSDGTGSDDKAKAGADGK-TKIATPRGAAPGQKQOANATRIIPAKTTP 177
 DB 80 GHYTOARMVSKSDGTGSDDKAKAGADGK-TKIATPRGAAPGQKQOANATRIIPAKTTP 139
 QY 178 APKTPSSGEPKSGDRSGYSSPGSPGTPGSRSPRLPTPTREPKKVAVVATPPKSPS 237
 DB 140 TPRTSP--GSGKSGDRSGYSSPGSPGTPGSRSPRLPTPTREPKKVAVVATPPKSPS 197
 QY 238 SAKSRLOTAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDLSNVQSKGSKDNI 297
 DB 198 SAKSRLOTAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDLSNVQSKGSKDNI 234
 QY 298 KAVPGGGSVOIYKPPVPLDKSVTSKCSGLNHHKPPGGGVYEVKSEKLDPRVQSKIGSL 357
 DB 235 -----VOIYKPPVPLDKSVTSKCSGLNHHKPPGGGVYEVKSEKLDPRVQSKIGSL 286
 QY 358 DNITHVPGGNNK 370
 DB 287 DNITHVPGGNNK 299

RESULT 12
 028189 PRELIMINARY; PRT; 316 AA.

ID 028189
 AC 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE TAU PROTEIN.
 GN TAU.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261765.
 RA HIMMER A.; DRECHSEL D.; KIRSCHNER M.W.; MARTIN D.W.;
 RT "Tau consists of a set of proteins with repeated C-terminal
 microtubule-binding domains and variable N-terminal domains."
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261766.
 RA HIMMER A.;
 RT "Structure of the bovine tau gene: alternatively spliced transcripts
 generate a protein family."
 RL Mol. Cell. Biol. 9:1389-1396(1989).
 DR EMBL: M26178; AAAS1606.1; JOINED.
 DR EMBL: L34940; AAAS1606.1; JOINED.
 DR EMBL: L34941; AAAS1606.1; JOINED.
 DR EMBL: L34944; AAAS1606.1; JOINED.
 DR EMBL: L34946; AAAS1606.1; JOINED.
 DR EMBL: L34948; AAAS1606.1; JOINED.
 DR EMBL: L34950; AAAS1606.1; JOINED.
 DR EMBL: L34951; AAAS1606.1; JOINED.
 DR PROSITE: P500229; TAU_MAP; 3.
 DR PFAM: PF00418; tubulin-binding; 3.
 KW Microtubules; Repeat.
 SQ SEQUENCE 316 AA; 32770 MW; DEC3A429 CRC32;

Query Match 53.5%; Score 1228.5; DB 6; Length 316;
 Best Local Similarity 68.4%; Pred. No. 1e-70; Indels 99; Gaps 6;
 Matches 255; Conservative 4; Mismatches 15;

QY 1 MAEPREFEWMEDHAGODTYGLDRKDGQGYTMH-OEGDTDAGLKESPLQTPTEDESGEEP 59
 DB 1 MAEPREFEWMEDHAGODTYGLDRKDGQGYTMH-OEGDTDAGLKESPLQTPTEDESGEEP 48
 QY 60 GSETSDAKSTPTAEADYTAFLVDEGAPGKQAAAPHTETPEGTAEAGIGDTPSLEDEA 119
 DB 49 GSETSDAKSTPTAEADYTAFLVDEGAPGKQAAAPHTETPEGTAEAGIGDTPSLEDEA 62
 QY 120 GHYTOARMVSKSDGTGSDDKAKAGADGK-TKIATPRGAAPGQKQOANATRIIPAKTTP 177
 DB 63 -----ARMVSKSDGTGSDDKAKAGADGK-TKIATPRGAAPGQKQOANATRIIPAKTTP 117
 QY 178 APKTPSSGEPKSGDRSGYSSPGSPGTPGSRSPRLPTPTREPKKVAVVATPPKSPS 237
 DB 118 TPRTSP--GSGKSGDRSGYSSPGSPGTPGSRSPRLPTPTREPKKVAVVATPPKSPS 175
 QY 238 SAKSRLOTAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDLSNVQSKGSKDNI 297
 DB 176 SAKSRLOTAPVPMPLDKNVKSKIGSTENLKHOPGGKVOIINKKLDLSNVQSKGSKDNI 212
 QY 298 KAVPGGGSVOIYKPPVPLDKSVTSKCSGLNHHKPPGGGVYEVKSEKLDPRVQSKIGSL 357
 DB 213 -----VOIYKPPVPLDKSVTSKCSGLNHHKPPGGGVYEVKSEKLDPRVQSKIGSL 264
 QY 358 DNITHVPGGNNK 370
 DB 265 DNITHVPGGNNK 277

RESULT 13
 064715 PRELIMINARY; PRT; 1825 AA.

ID 064715
 AC 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE MICROTUBULE ASSOCIATED PROTEIN 2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RA DRESSE A.E.;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1802-1825 FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE: 89334524.
 RA MARECHAL D.; DELAPOERRE D.; DRESSE A.;
 RT "Cloning and partial sequencing of a new rat brain specific cDNA."
 RL Arch. Int. Physiol. Biochim. 96:231-236(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-BRAIN;
 RX MEDLINE: 95094034.
 RA FERHAT L.; BEN-ART Y.P.; KHRESTCHATISKY M.;
 RT "Complete sequence of rat MAP2d, a novel MAP2 isoform."
 RL C. R. Acad. Sci., III, Sci. Vie 317:304-309(1994).
 DR EMBL: X54100; CAA38034.1; -.
 DR EMBL: X74211; CAA52283.1; -.
 DR PROSITE: P500229; TAU_MAP; 2.
 DR PFAM: PF00418; tubulin-binding; 3.
 KW Microtubules; Repeat.
 FT CONFLICT 151 1509 MISSING (IN REF. 3).
 FT CONFLICT 1689 1689 O -> VRLINKIDSKVQSGSKDNKHSAGGN
 FT (IN REF. 3).
 SQ SEQUENCE 1825 AA; 198565 MW; AB7B2EAB CRC32;

CC OF MICROTUBULES DURING DIFFERENT STAGES OF NEURONAL DEVELOPMENT.
 CC THE VARYING LENGTH OF THE PROJECTION ARM SERVES AS A SPACER
 CC BETWEEN MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: AS IN OTHER MAMMALS, SEVERAL ISOFORMS
 CC INCLUDING ONE POSSESSING AN ADDITIONAL TAU/MAP REPEAT, MIGHT BE
 CC PRODUCED BY DEVELOPMENTALLY CONTROLLED ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN. THE SECOND REPEAT
 CC PLAYS A DOMINANT ROLE IN MICROTUBULE BINDING.
 CC -1- PTM: PHOSPHORYLATION AT VARIOUS SITES IN THE N-TERMINAL BY A CAMP-
 CC DEPENDENT PROTEIN KINASE (PKA), IN THE PROLINE-RICH C-TERMINAL
 CC DOMAIN BY PROLINE-DIRECTED PROTEIN KINASES (CDC2, GSK3) AND OF
 CC SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-
 CC REGULATING KINASE (MARK). IN VITRO, PHOSPHORYLATION BY PKA AFFECTS
 CC THE MICROTUBULE-ASSEMBLING ACTIVITY, BY CDC2 AFFECTS BOTH THE
 CC MICROTUBULE-ASSEMBLING AND STABILIZING ACTIVITY OF MAP2.
 CC PHOSPHORYLATION BY MARK DECREASES TUBULIN-BINDING AND MICROTUBULES
 CC ASSEMBLY, ALLOWING THE REARRANGEMENT OF THE MICROTUBULE NETWORK.
 CC -1- PTM: THE N-TERMINAL IS BLOCKED.
 CC -1- MISCELLANEOUS: MUTAGENESIS EXPERIMENTS WERE DONE IN REF.1 IN WHICH
 CC THE FIRST AND THIRD REPEATS WERE MODIFIED TO RESEMBLE THE SECOND
 CC REPEAT WHICH LEAD TO SOMEWHAT HIGHER AFFINITY MICROTUBULE BINDING.
 CC -1- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS, FROM WHICH ONE IS
 CC APPROXIMATE.
 DR EMBL; S74025; AAB32526.1; ALT_SEQ.
 DR PROSITE; PS00229; TAU_MAP; 2.
 DR PFM; PF00418; tubulin-binding; 3.
 KW Microtubules; Repeat; Alternative splicing; Cytoskeleton;
 KM Phosphorylation.
 FT NON_TER 1 1
 FT REPEAT 156 187 TAU/MAP MOTIF.
 FT REPEAT 188 218 TAU/MAP MOTIF.
 FT REPEAT 219 250 TAU/MAP MOTIF.
 FT REPEAT 251 282 APPROXIMATE TAU/MAP MOTIF.
 FT MOD_RES 37 37 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 FT MOD_RES 109 109 PHOSPHORYLATION (BY A PROLINE-DIRECTED
 FT KINASE) (BY SIMILARITY).
 FT MOD_RES 112 112 PHOSPHORYLATION (BY A PROLINE-DIRECTED
 FT KINASE) (BY SIMILARITY).
 FT MOD_RES 115 115 PHOSPHORYLATION (BY A PROLINE-DIRECTED
 FT KINASE) (BY SIMILARITY).
 FT MOD_RES 175 175 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 FT MOD_RES 206 206 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 FT MOD_RES 238 238 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD_RES 291 291 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 FT MOD_RES 295 295 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 FT MOD_RES 298 298 PHOSPHORYLATION (BY MARK) (BY
 FT SIMILARITY).
 SQ SEQUENCE 323 AA; 34131 MM; 43FD17F CRC32;

Query Match 30.9%; Score 710; DB 6; Length 323;
 Best Local Similarity 44.4%; Pred. No. 5.9e-38;
 Matches 164; Conservative 51; Mismatches 78; Indels 76; Gaps 10;

OY 101 TTAETAGTGTPEDEAGHYTAQAMYSKSDG-----TGSDDKAK 143
 DB 3 TTAAGAESQAQAPSVFKQAKDKVSDG-VTKSPKRSILPRPSILPRRGVSGDRDENSEF 60
 OY 144 GADGTXATATRGAAAP-----GKGQANATRIAPKTPAPKTPSSGSEPPKSGDRSGYSS 199
 DB 61 SLNSGISARRTTRSEPIRRAGKSGTSTPT-TPGSTAITPGPPS-----YSS 107
 OY 200 --PGSPGTGSGRSRTSLPTPP-----TRPKYAVVTRTPKSPSSAKSLQATAPVPMAPD 252
 DB 108 RTPGPGRFP-SYPRPPTHPGTPKSAIIVPSEKVAIIRTPKSPATPK-QLRLINQPLPD 165
 OY 253 LKNYKSKIGSTENLKHQGGGKVOIINKKLDSNVQSKGSKDNIKHVPGGGVOIYTKP 312
 |||||

DB 166 LKNYKSKIGSTDNIKYQPKGGVOIYTKKIDLSH----- 199
 OY 313 VDLKRYTSKGSGLNHHKPGGGVEYKSEKLDKDRVQSKIGSLDNIHYVGGGNKIE 372
 DB 200 ----VTSKGSGLNHHKPGGGVKIESVYLDPEKKAQAQVSLDNAHVPGGGNKID 254
 OY 373 THKTFENAKAKTDGAEIYKSPVYSGDTSFPHLSNVSTGSDIWDVDFQLATLDEV 432
 DB 255 SQKLNFREHAKARVDGAEITQSPGRSVASPPRLSNVSSGSLNLESPOLATLAEV 314
 OY 433 SASLAKGL 441
 DB 315 TALAKGL 323

Search completed: September 28, 2000, 20:03:00
 Job time: 276 sec

Fri Sep 29 08:18:21 2000

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